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(54) Title: NOVEL COMPOUNDS

(57) Abstract: Polypeptides and polynucleotides of the genes set forth in Table I and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing polypeptides and polynucleotides of the genes set forth in Table I in diagnostic assays.

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## **Novel Compounds**

### **Field of Invention**

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides. The polynucleotides and polypeptides of the present invention also relate to proteins with signal sequences which allow them to be secreted extracellularly or membrane-associated (hereinafter often referred collectively as secreted proteins or secreted polypeptides).

### **Background of the Invention**

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superseding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Proteins and polypeptides that are naturally secreted into blood, lymph and other body fluids, or secreted into the cellular membrane are of primary interest for pharmaceutical research and development. The reason for this interest is the relative ease to target protein therapeutics into their place of action (body fluids or the cellular membrane). The natural pathway for protein secretion into extracellular space is the endoplasmic reticulum in eukaryotes and the inner membrane in prokaryotes (Palade, 1975, Science, 189, 347; Milstein, Brownlee, Harrison, and Mathews, 1972, Nature New Biol., 239, 117; Blobel, and Dobberstein, 1975, J. Cell. Biol., 67, 835). On the other hand, there is no known natural pathway for exporting a protein from the exterior of the cells into the cytosol (with the exception of pinocytosis, a mechanism of snake venom toxin intrusion into cells). Therefore targeting protein therapeutics into cells poses extreme difficulties.

The secreted and membrane-associated proteins include but are not limited

to all peptide hormones and their receptors (including but not limited to insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic hormones, neuropsin, neurotrophins, pituitary hormones, pleiotropins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins), the breast and colon cancer gene products, leptin, the obesity gene protein and its receptors, serum albumin, superoxide dismutase, spliceosome proteins, 7TM (transmembrane) proteins also called as G-protein coupled receptors, immunoglobulins, several families of serine proteinases (including but not limited to proteins of the blood coagulation cascade, digestive enzymes), deoxyribonuclease I, etc.

Therapeutics based on secreted or membrane-associated proteins approved by FDA or foreign agencies include but are not limited to insulin, glucagon, growth hormone, chorionic gonadotropin, follicle stimulating hormone, luteinizing hormone, calcitonin, adrenocorticotrophic hormone (ACTH), vasopressin, interleukines, interferones, immunoglobulins, lactoferrin (diverse products marketed by several companies), tissue-type plasminogen activator (Alteplase by Genentech), hyaluronidase (Wydase by Wyeth-Ayerst), dornase alpha (Pulmozyme by Genentech), Chymodiactin (chymopapain by Knoll), alglucerase (Ceredase by Genzyme), streptokinase (Kabikinase by Pharmacia) (Streptase by Astra), etc. This indicates that secreted and membrane-associated proteins have an established, proven history as therapeutic targets. Clearly, there is a need for identification and characterization of further secreted and membrane-associated proteins which can play a role in preventing, ameliorating or correcting dysfunction or disease, including but not limited to diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The proteins of the present invention which include the signal sequences are also useful to further elucidate the mechanism of protein transport which at present is not entirely understood, and thus can be used as research tools.

### Summary of the Invention

The present invention relates to particular polypeptides and polynucleotides of the genes set forth in Table I, including recombinant materials and methods for their production.

Such polypeptides and polynucleotides are of interest in relation to methods of treatment of certain diseases, including, but not limited to, the diseases set forth in Tables III and V, hereinafter referred to as "diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (*e.g.*, inhibitors) using the materials provided by the invention, and treating conditions associated with imbalance of polypeptides and/or polynucleotides of the genes set forth in Table I with the identified compounds. In still a further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels the genes set forth in Table I. Another aspect of the invention concerns a polynucleotide comprising any of the nucleotide sequences set forth in the Sequence Listing and a polypeptide comprising a polypeptide encoded by the nucleotide sequence. In another aspect, the invention relates to a polypeptide comprising any of the polypeptide sequences set forth in the Sequence Listing and recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such polypeptides and polynucleotides. Such uses include the treatment of diseases, abnormalities and disorders (hereinafter simply referred to as diseases) caused by abnormal expression, production, function and or metabolism of the genes of this invention, and such diseases are readily apparent by those skilled in the art from the homology to other proteins disclosed for each attached sequence. In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with the imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels of the secreted proteins of the present invention.

## **Description of the Invention**

In a first aspect, the present invention relates to polypeptides the genes set forth in Table I. Such polypeptides include:

- (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in the Sequence Listing, herein when referring to polynucleotides or polypeptides of the Sequence Listing, a reference is also made to the Sequence Listing referred to in the Sequence Listing;
- (b) an isolated polypeptide comprising a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (c) an isolated polypeptide comprising a polypeptide sequence set forth in the Sequence Listing;



- (d) an isolated polypeptide having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (e) a polypeptide sequence set forth in the Sequence Listing; and
- (f) an isolated polypeptide having or comprising a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing;
- (g) fragments and variants of such polypeptides in (a) to (f).

Polypeptides of the present invention are believed to be members of the gene families set forth in Table II. They are therefore of therapeutic and diagnostic interest for the reasons set forth in Tables III and V. The biological properties of the polypeptides and polynucleotides of the genes set forth in Table I are hereinafter referred to as "the biological activity" of polypeptides and polynucleotides of the genes set forth in Table I. Preferably, a polypeptide of the present invention exhibits at least one biological activity of the genes set forth in Table I.

Polypeptides of the present invention also include variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from an amino acid sequence set forth in the Sequence Listing, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from an amino acid sequence set forth in the Sequence Listing. Preferred fragments are biologically active fragments that mediate the biological activity of polypeptides and polynucleotides of the genes set forth in Table I, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of a polypeptide of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention. A polypeptide of the present invention may be in the form of the "mature" protein or may be a

part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5            Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation from naturally occurring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance automated peptide synthesizers, or a combination of such methods. Means for preparing such polypeptides are well understood in the art.
- 10        In a further aspect, the present invention relates to polynucleotides of the genes set forth in Table I. Such polynucleotides include:
- (a) an isolated polynucleotide comprising a polynucleotide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide sequence set forth in the Sequence Listing;
  - 15        (b) an isolated polynucleotide comprising a polynucleotide set forth in the Sequence Listing;
  - (c) an isolated polynucleotide having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide set forth in the Sequence Listing;
  - (d) an isolated polynucleotide set forth in the Sequence Listing;
  - 20        (e) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
  - (f) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing;
  - 25        (g) an isolated polynucleotide having a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
  - (h) an isolated polynucleotide encoding a polypeptide set forth in the Sequence Listing;
  - (i) an isolated polynucleotide having or comprising a polynucleotide sequence that has an
  - 30        Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polynucleotide sequence set forth in the Sequence Listing;
  - (j) an isolated polynucleotide having or comprising a polynucleotide sequence encoding a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing; and

polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide comprising an nucleotide sequence having at least 15, 30, 50 or 100  
5 contiguous nucleotides from a sequence set forth in the Sequence Listing, or an isolated polynucleotide comprising a sequence having at least 30, 50 or 100 contiguous nucleotides truncated or deleted from a sequence set forth in the Sequence Listing.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more  
10 single nucleotide polymorphisms (SNPs).

Polynucleotides of the present invention also include polynucleotides encoding polypeptide variants that comprise an amino acid sequence set forth in the Sequence Listing and in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acid residues are substituted, deleted or  
15 added, in any combination.

In a further aspect, the present invention provides polynucleotides that are RNA transcripts of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide that:

(a) comprises an RNA transcript of the DNA sequence encoding a polypeptide set forth in the Sequence Listing;  
20

(b) is a RNA transcript of a DNA sequence encoding a polypeptide set forth in the Sequence Listing;

(c) comprises an RNA transcript of a DNA sequence set forth in the Sequence Listing; or

25 (d) is a RNA transcript of a DNA sequence set forth in the Sequence Listing; and RNA polynucleotides that are complementary thereto.

The polynucleotide sequences set forth in the Sequence Listing show homology with the polynucleotide sequences set forth in Table II. A polynucleotide sequence set forth in the Sequence Listing is a cDNA sequence that encodes a polypeptide set forth in the  
30 Sequence Listing. A polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing may be identical to a polypeptide encoding a sequence set forth in the Sequence Listing or it may be a sequence other than a sequence set forth in the Sequence Listing, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes a polypeptide set forth in the Sequence Listing. A polypeptide of a sequence set forth in the  
35 Sequence Listing is related to other proteins of the gene families set forth in Table II, having

homology and/or structural similarity with the polypeptides set forth in Table II. Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one activity of the genes set forth in Table I.

Polynucleotides of the present invention may be obtained using standard cloning and screening techniques from a cDNA library derived from mRNA from the tissues set forth in Table IV (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. A polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide sequence set forth in the Sequence Listing, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from other species) that have a high sequence similarity to sequences set forth in the Sequence Listing, typically at least 95% identity. Preferred probes and primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between

30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from other species, may be obtained by a process comprising the steps of  
5 screening a library under stringent hybridization conditions with a labeled probe having a sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing the polynucleotide sequence set forth in the Sequence Listing. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include  
10 overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100,  
15 obtained by screening a library under stringent hybridization conditions with a labeled probe having the sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way  
20 through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to  
25 obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark)  
30 technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an  
35 adapter specific primer that anneals further 3' in the adaptor sequence and a gene specific

primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al. (ibid)*. Preferred methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, micro-injection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a

polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of a gene is characterized by the polynucleotides set forth in the Sequence Listing in the cDNA or genomic sequence and which is associated with a dysfunction. Will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified

by hybridizing amplified DNA to labeled nucleotide sequences of the genes set forth in Table I. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401).

An array of oligonucleotides probes comprising polynucleotide sequences or fragments thereof of the genes set forth in Table I can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M. Chee *et al.*, Science, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subject to a disease of the invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radio-immunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit comprising:

- (a) a polynucleotide of the present invention, preferably the nucleotide sequence set forth in the Sequence Listing, or a fragment or an RNA transcript thereof;
- (b) a nucleotide sequence complementary to that of (a);
- (c) a polypeptide of the present invention, preferably the polypeptide set forth in the Sequence Listing or a fragment thereof; or
- (d) an antibody to a polypeptide of the present invention, preferably to the polypeptide set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.



The polynucleotide sequences of the present invention are valuable for chromosome localisation studies. The sequences set forth in the Sequence Listing are specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (co-inheritance of physically adjacent genes). Precise human chromosomal localisations for a genomic sequence (gene fragment etc.) can be determined using Radiation Hybrid (RH) Mapping (Walter, M. Spillett, D., Thomas, P., Weissenbach, J., and Goodfellow, P., (1994) A method for constructing radiation hybrid maps of whole genomes, *Nature Genetics* 7, 22-28). A number of RH panels are available from Research Genetics (Huntsville, AL, USA) e.g. the GeneBridge4 RH panel (*Hum Mol Genet* 1996 Mar;5(3):339-46 A radiation hybrid map of the human genome. Gyapay G, Schmitt K, Fizames C, Jones H, Vega-Czarny N, Spillett D, Muselet D, Prud'Homme JF, Dib C, Auffray C, Morissette J, Weissenbach J, Goodfellow PN). To determine the chromosomal location of a gene using this panel, 93 PCRs are performed using primers designed from the gene of interest on RH DNAs. Each of these DNAs contains random human genomic fragments maintained in a hamster background (human / hamster hybrid cell lines). These PCRs result in 93 scores indicating the presence or absence of the PCR product of the gene of interest. These scores are compared with scores created using PCR products from genomic sequences of known location. This comparison is conducted at <http://www.genome.wi.mit.edu/>.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include in situ hybridization techniques to clones arrayed on a grid, such as cDNA microarray hybridization (Schena *et al*, *Science*, 270, 467-470, 1995 and Shalon *et al*, *Genome Res*, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an

indication of the normal function of the polypeptide in the organism. In addition, comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells,

to protect said animal from disease, whether that disease is already established within the individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce  
5 such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The  
10 formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intra-muscular, intravenous, or intra-dermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation isotonic with the  
15 blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the  
20 immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention  
25 hereinbefore mentioned. It is therefore useful to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such  
30 diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections of chemical compounds, and natural product mixtures. Such agonists or antagonists so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule. Such  
35

small molecules preferably have a molecular weight below 2,000 daltons, more preferably between 300 and 1,000 daltons, and most preferably between 400 and 700 daltons. It is preferred that these small molecules are organic molecules.

5 The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test 10 whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate 15 compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring an activity of the genes set forth in Table I in the mixture, and comparing activity of the mixture of the genes set forth in Table I to a control mixture which contains no candidate compound.

20 Polypeptides of the present invention may be employed in conventional low capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well micotiter plates but also emerging methods such as the nanowell method described by Schullek et al, *Anal Biochem.*, 246, 20-29, (1997).

25 Fusion proteins, such as those made from Fc portion and polypeptide of the genes set forth in Table I, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, *J Mol Recognition*, 8:52-58 (1995); and K. Johanson *et al.*, *J Biol Chem*, 270(16):9459-9471 (1995)).

30 The polynucleotides, polypeptides and antibodies to the polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide 35 (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance,  $^{125}\text{I}$ ), chemically modified  
5 (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of  
10 the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment  
15 of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and the genes set forth in Table I. The art of constructing transgenic animals is well established. For  
20 example, the genes set forth in Table I may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation embryos, or injection of genetically modified, such as by electroporation, embryonic stem cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of  
25 that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific  
30 cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic animal technology also offers a whole animal expression-cloning system in which introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

- (a) a polypeptide of the present invention;
  - (b) a recombinant cell expressing a polypeptide of the present invention;
  - 5 (c) a cell membrane expressing a polypeptide of the present invention; or
  - (d) an antibody to a polypeptide of the present invention;
- which polypeptide is preferably that set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

10

### Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

- “Antibodies” as used herein includes polyclonal and monoclonal antibodies, chimeric,  
15 single chain, and humanized antibodies, as well as Fab fragments, including the products of an  
Fab or other immunoglobulin expression library.

- “Isolated” means altered “by the hand of man” from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For  
20 example, a polynucleotide or a polypeptide naturally present in a living organism is not  
“isolated,” but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is “isolated”, as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is “isolated” even if it is still present in  
25 said organism, which organism may be living or non-living.

- “Secreted protein activity or secreted polypeptide activity” or “biological activity of the secreted protein or secreted polypeptide” refers to the metabolic or physiologic function of said secreted protein including similar activities or improved activities or these activities with decreased undesirable side-effects. Also included are antigenic and immunogenic  
30 activities of said secreted protein.

“Secreted protein gene” refers to a polynucleotide comprising any of the attached nucleotide sequences or allelic variants thereof and/or their complements.

“Polynucleotide” generally refers to any polyribonucleotide (RNA) or polydeoxribonucleotide (DNA), which may be unmodified or modified RNA or DNA.

- 35 “Polynucleotides” include, without limitation, single- and double-stranded DNA, DNA that

is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-  
5 stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically,  
10 enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined  
15 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational  
20 processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the  
25 same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-  
30 ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation,  
35 glycosylation, GPI anchor formation, hydroxylation, iodination, methylation,

myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, *Proteins - Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, 1-12, in *Post-translational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol*, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci*, 663, 48-62, 1992).

5 "Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucleotide sequence that is shorter than the reference sequence set forth in the Sequence Listing.

15 "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes  
20 may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide  
25 may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not  
30 known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like. Embodiments include methylation of the N-terminal amino acid, phosphorylations of  
35 serines and threonines and modification of C-terminal glycines.



"Allele" refers to one of two or more alternative forms of a gene occurring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

5 "Single Nucleotide Polymorphism" (SNP) refers to the occurrence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This  
10 common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are identical to each other except that the final 3' base wobbles to match one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

15 "Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid  
20 sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid  
25 correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

"% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in  
30 either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences  
5 being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are  
10 well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences.  
15 BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP  
20 aligns two sequences, finding a "maximum similarity", according to the algorithm of Neddleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences,  
25 respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997,  
30 available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448,1988, available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

5        Preferably, the program BESTFIT is used to determine the % identity of a query polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a polypeptide sequence, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

      "Identity Index" is a measure of sequence relatedness which may be used to  
10       compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence. Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference sequence except that the candidate polynucleotide sequence may include on average up to  
15       five differences per each 100 nucleotides of the reference sequence. Such differences are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between these terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to  
20       obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference polynucleotide sequence, an average of up to 5 in every 100 of the nucleotides of the in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

25       Similarly, for a polypeptide, a candidate polypeptide sequence having, for example, an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the reference sequence except that the polypeptide sequence may include an average of up to five differences per each 100 amino acids of the reference sequence. Such differences are selected from the group consisting of at least one amino acid deletion, substitution,  
30       including conservative and non-conservative substitution, or insertion. These differences may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between these terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polypeptide sequence having an  
35       Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5

in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$n_a \leq x_a - (x_a \cdot I),$$

in which:

$n_a$  is the number of nucleotide or amino acid differences,

$x_a$  is the total number of nucleotides or amino acids in a sequence set forth in the

Sequence Listing,

$I$  is the Identity Index,

$\cdot$  is the symbol for the multiplication operator, and

in which any non-integer product of  $x_a$  and  $I$  is rounded down to the nearest integer prior to subtracting it from  $x_a$ .

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotide or polypeptide that within the same species which is functionally similar.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 533-A discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, *e.g.*, EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which

this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

**Table I**

Gene Name	GSK Gene ID	Nucleic Acid SEQ ID NO's	Corresponding Protein SEQ ID NO's
sbg458463PERLAXINa	458463	SEQ ID NO:1 SEQ ID NO:2	SEQ ID NO:29 SEQ ID NO:30
sbg507885RDPa	507885	SEQ ID NO:3 SEQ ID NO:4	SEQ ID NO:31 SEQ ID NO:32
sbg507885RDPb	507885	SEQ ID NO:5	SEQ ID NO:33
SBh511364.NR-CAMa	511364	SEQ ID NO:6 SEQ ID NO:7	SEQ ID NO:34 SEQ ID NO:35
SBh511364.NR-CAMb	511364	SEQ ID NO:8	SEQ ID NO:36
SBh511827.C1q-related factor	511827	SEQ ID NO:9 SEQ ID NO:10	SEQ ID NO:37 SEQ ID NO:38
sbg533677PALSa	533677	SEQ ID NO:11 SEQ ID NO:12	SEQ ID NO:39 SEQ ID NO:40
sbg535067MELAAa	535067	SEQ ID NO:13	SEQ ID NO:41
sbg590979THP	590979	SEQ ID NO:14 SEQ ID NO:15	SEQ ID NO:42 SEQ ID NO:43
sbg658629CRF	658629	SEQ ID NO:16 SEQ ID NO:17	SEQ ID NO:44 SEQ ID NO:45
sbg507131mannosidase	507131	SEQ ID NO:18 SEQ ID NO:19	SEQ ID NO:46 SEQ ID NO:47
sbg655871calgizzarin- like	655871	SEQ ID NO:20 SEQ ID NO:21	SEQ ID NO:48 SEQ ID NO:49
sbg506454MPG-1	506454	SEQ ID NO:22 SEQ ID NO:23	SEQ ID NO:50 SEQ ID NO:51
sbg659837OBCAM	659837	SEQ ID NO:24 SEQ ID NO:25	SEQ ID NO:52 SEQ ID NO:53
sbg467870CBP	467870	SEQ ID NO:26	SEQ ID NO:54
sbg514112RNase	514112	SEQ ID NO:27	SEQ ID NO:55
sbg962274FGF-BP	962274	SEQ ID NO:28	SEQ ID NO:56

Table II

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg458463 PERLAXI Na	Periaxin protein	GB:AC010271 Submitted (15-SEP-1999) by Production Sequencing Facility, DOE Joint Genome Institute	Human periaxin, gi:13649706 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Cytosolic
sbg507885 RDPa	Renal dipeptidase	JGI:RPCI-11_331B16 Found at Joint Genome Institute, Department of Energy, USA	Human putative metallopeptidase (family M19), gi:11641273 Submitted (02-NOV-2000) by Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UNITED KINGDOM	Secreted
sbg507885 RDPb	Renal dipeptidase	JGI:RPCI-11_331B16 Found at Joint Genome Institute, Department of Energy, USA	Human putative metallopeptidase (family M19), gi:11641273 Submitted (02-NOV-2000) by Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UNITED KINGDOM	Secreted
SBh511364 .NR-CAMa	Immuno- globulin superfam- ily, neuron- glia cell adhesion molecule- related protein (Nr- CAM)	EMBL:AC073550 Submitted (22-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human hypothetical protein, gi:6807875 Submitted (15-JAN-2000) MIPS, Am Klopferspitze 18a, D-82152 Martinsried, GERMANY	Membrane-bound
SBh511364 .NR-CAMb	Neuron- glia cell adhesion molecule- related protein (Nr- CAM)	EMBL:AC073550 Submitted (22-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human hypothetical protein, gi:13632065 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Cytosolic
SBh511827 .C1q- related factor	Comple- ment-c1q tumor necrosis factor- related protein	GB:AC026707 Submitted (23-MAR- 2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,	Human complement-c1q tumor necrosis factor-related protein, gi: 13569919 Maeda T, Abe M, Kurisu K, Jikko A and Furukawa S J Biol Chem 2001 Feb 2;276(5):3628-34	Secreted

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Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg533677 PALSa	Palmitoylated 3 (MAGUK p55 subfamily member 5, proteins associated with Lin-7 (PALs))	GB:AL135978 Submitted (15-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE	Mouse palmitoylated 3 (MAGUK p55 subfamily member 5), gi: 9625023 Kamberov,E., Makarova,O., Roh,M., Liu,A., Karnak,D., Straight,S. and Margolis,B. J. Biol. Chem. 275 (15), 11425-11431 (2000).	Membrane-bound
sbg535067 MELAa	Melanoma associated protein	SC:AL096827 Submitted (13-SEP-1999) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Unidentified human gene, gi:10047249 Submitted (03-AUG-2000) by Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan	Membrane-bound
sbg590979 THP	Tamm-Horsfall protien (THP)	GB: AC069548 Direct submitted (02-JUN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA	Human pancreatic zymogen granule membrane protein GP2, gi:4504075 Wong,S.M. and Lowe,A.W. Gene 171 (2), 311-312 (1996)	Secreted
sbg658629 CRF	C1q-related factor	GB:AC010173 Direct submitted (15-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX77030, USA	Human C1q-related factor, gi :5729785 Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR and Pereira-Smith OM. Brain Res. Mol. Brain Res. 63 (2), 233-240 (1999)	Secreted
sbg507131 mannosidase	Alpha-mannosidase	GB:AC004480 Direct submitted (27-MAR-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA.	Mouse mannosidase 2, alpha B2, gi:6678792 Hiramoto,S., Tamba,M., Kiuchi,S., Jin,Y.Z., Bannai,S., Sugita,Y., Dacheux,F., Dacheux,J.L., Yoshida,M. and Okamura,N. Biochem. Biophys. Res. Commun. 241 (2), 439-445 (1997)	Secreted



Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg655871 calgizzarin-like	S100 calcium-binding protein	GB:AC027667 Direct submitted (01-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Mouse calgizzarin (endothelial monocyte-activating polypeptide), gi: 1710819, Fan, Y., Leung, D., Houck, K.A., Yan, S., Brett, J., Heath, M., Pan, Y., Clauss, M., Kisiel, W., Chabot, J., Logerfo, P., Stern, D. and Kao, J. submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases	Secreted
sbg506454 MPG-1	Macrophage Gene-1 Product (MGP1)	GB:AP000406 Submitted (27-AUG-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan	Mouse MPS1 protein gi:2137564 Spilsbury, K., O'Mara, M.A., Wu, W.M., Rowe, P.B., Symonds, G. and Takayama, Y. Blood 85 (6), 1620-1629 (1995)	Secreted
sbg659837 OBCAM	Opioid-binding cell adhesion molecule (OBCAM)	GB: AC016769 Submitted (25-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Bovine opioid-binding cell adhesion molecule Schofield, P.R., McFarland, K.C., Hayflick, J.S., Wilcox, J.N., Cho, T.M., Roy, S., Lee, N.M., Loh, H.H. and Seeburg, P.H. EMBO J. 8 (2), 489-495 (1989)	Secreted
sbg467870 CBP	EF-hand protein	GB:AC018638 Direct submitted (15-DEC-1999) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA.	Rat CBP-50 protein, gi:2511701 Submitted (04-OCT-1997) by Hseu M.J., Institute of Biological Chemistry, Academia Sinica, Taiwan, R. O. C., P.O.Box 23-106, Taipei, Taiwan, 10098, REPUBLIC OF CHINA	Endoplasmic reticulum-bound (secreted if C-terminus HDEF were deleted)
sbg514112 RNase	RNase	GB:AL355075 Direct submitted (06-JUN-2000) to the EMBL/GenBank/DDBJ databases by Genoscope.	Mouse putative protein, gi: 12853968 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Genome Res. 10 (10), 1617-1630 (2000)	Secreted

Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg962274 FGF-BP	Fibroblast growth factor binding protein	EMBL:AL359198 Found at Sanger Centre and submitted (08-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Mouse putative protein, gi: 12853968 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Genome Res. 10 (10), 1617-1630 (2000)	Secreted

Table III

Gene Name	Uses	Associated Diseases
sbg458463 PERLAXI Na	An embodiment of the invention is the use of sbg458463PERLAXINa in axon-glial interactions. A close homologue of sbg458463PERLAXINa is the rat periaxin (PRX). Rat periaxin (PRX), a protein of myelinating Schwann cells. Periaxin has a role in axon-glial interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin-associated glycoprotein in the periaxonal regions of the Schwann cell plasma membrane (Gillespie CS, Sherman DL, Blair GE, Brophy PJ. Periaxin, a protein of myelinating Schwann cells with a possible role in axonal ensheathment. Neuron 1994 Mar;12(3):497-508). Prx(-/-) mice develop a severe demyelinating peripheral neuropathy, despite apparently normal initial formation of myelin sheaths. Three unrelated Dejerine-Sottas neuropathy patients with recessive PRX mutations have been identified. It was hypothesized that mutations in PRX could cause human peripheral myelinopathies (Boerkoel,C.F., Takashima,H., Stankiewicz,P., Garcia,C.A., Leber,S.M., Rhee-Morris,L. and Lupski,J.R. Am. J. Hum. Genet. 68 (2), 325-333 (2001)).	Peripheral myelinopathies, infection, cancer, autoimmune disorders, wound healing disorders and hematopoietic disorders
sbg507885 RDPa	An embodiment of the invention is the use of sbg507885RDPa in the renal metabolism. Close homologues of sbg507885RDPa are microsomal dipeptidases. The renal dipeptidase (RDP), previously referred to as microsomal dipeptidase, is a kidney membrane enzyme which hydrolyzes a variety of dipeptides, and is implicated in the renal metabolism. RDP is responsible for hydrolysis of the beta-lactam ring of antibiotics (Campbell BJ, Forrester LJ, Zahler WL, Burks M; 1984; Biol Chem 259:14586-90). The renal dipeptidase has been shown to be a glycosylphosphatidylinositol-anchored ectoenzyme within the renal proximal tubules, and is proposed as a diagnostic enzyme of renal disease (Kang BY, We JS, Choi K, Lee HB, Han HJ, Park H; 1999; Arch Pharm Res 22:367-71).	Cancer, infection, autoimmune disorder, inflammation, and acute renal failure
sbg507885 RDPb	An embodiment of the invention is the use of sbg507885RDPb in the renal metabolism. Close homologues of sbg507885RDPb are microsomal dipeptidases. The renal dipeptidase (RDP), previously referred to as microsomal dipeptidase, is a kidney membrane enzyme which hydrolyzes a variety of dipeptides, and is implicated in the renal metabolism. RDP is responsible for hydrolysis of the beta-lactam ring of antibiotics (Campbell BJ, Forrester LJ, Zahler WL, Burks M; 1984; Biol Chem 259:14586-90). The renal dipeptidase has been shown to be a glycosylphosphatidylinositol-	Cancer, infection, autoimmune disorder, inflammation, and acute renal failure

	anchored ectoenzyme within the renal proximal tubules, and is proposed as a diagnostic enzyme of renal disease (Kang BY, We JS, Choi K, Lee HB, Han HJ, Park H; 1999; Arch Pharm Res 22:367-71).	
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**Table III (cont).**

Gene Name	Uses	Associated Diseases
SBh511364.NR-CAMa	An embodiment of the invention is the use of SBh511364.NR-CAMa in the pathogenesis and invasive/metastatic behavior of pancreatic cancers. A close homologue of SBh511364.NR-CAMa is neural cell adhesion molecule Nr-CAM protein. Nr-CAM protein has been detected in the brain and normal human pancreas. Its expression was markedly up-regulated in intraductal hyperplasia. Expression was well maintained in well or moderately differentiated carcinoma but was reduced or absent from most poorly differentiated tumors. In addition, 4 of 4 human pancreatic adenocarcinoma cell lines tested demonstrated little or no Nr-CAM expression. This differential regulation of Nr-CAM expression suggests that it may be involved in the pathogenesis and invasive/metastatic behavior of pancreatic cancers (Dhodapkar KM, Friedlander D, Scholes J, Grumet M. Hum Pathol 2001 Apr;32(4):396-400).	Cancer such as pancreatic cancers, infections, autoimmune diseases, and neurological disorders
SBh511364.NR-CAMb	An embodiment of the invention is the use of SBh511364.NR-CAMb as a marker for diagnosing, treating, inhibiting or preventing malignancies like brain cancer, leukemia, B cell lymphoma, premalignant conditions, benign tumors, hyperproliferative disorders or benign dysproliferative disorders. Similar protein's treatment is especially useful for treating glioblastoma, glioma, meningioma, astrocytoma, medulloblastoma, neuroectodermal cancer and neuroblastoma, especially glioblastoma multiforme (WO9955380-A1, 04-NOV-99; Boynton AI, Murphy Gp, Sehgal A. Pacific Northwest Cancer Foundation).	Hematopoietic disorder, wound healing disorders, autoimmune diseases, viral and bacterial infections, cancer such as meningioma, astrocytoma, medulloblastoma, neuroectodermal and neuroblastoma, especially glioblastoma
SBh511827.C1q-related factor	An embodiment of the invention is the use of SBh511827.C1q-related factor in diagnosing and treating lung cancer and neurological disorders such as Parkinson's disease, Alzheimer's disease and schizophrenia as well as . A close homologue of SBh511827.C1q-related factor is collagenous repeat-containing sequence of 26-kDa protein (CORS26). Northern blot analysis revealed that CORS26 mRNA was present at high levels in rib growth plate cartilage and at moderate levels in kidney of adult mice. High levels of CORS26 mRNA were also detected in condensed prechondrocytic cells of cartilage primordia and developing cartilages in mouse embryos between 13 and 15 days postcoitus. Overexpression of CORS26 enhanced the growth of C3H10T1/2 cells in vitro. These data suggested that the CORS26 gene might play an important role in skeletal development. Related polypeptides have been reported useful for diagnosing and treating lung cancer (WO199938973-A2, FRUDAKIS TN, LODES MJ, MOHAMATH R, REED SG; 05-AUG-99; (CORI-) CORIXA CORP), and neurological disorders such as Parkinson's disease, Alzheimer's disease and schizophrenia (WO199942576-A1,	Hematopoietic disorder, skeletal development disorder, wound healing disorders, autoimmune diseases, viral and bacterial infections, lung tumor, cancer and growth abnormalities, parkinson's disease, alzheimer's disease and schizophrenia

	BARNES MR, 26-AUG-99;(SMIK ) SMITHKLINE BEECHAM PL.	
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Table III (cont).

Gene Name	Uses	Associated Diseases
sbg533677 PALSa	An embodiment of the invention is the use of sbg533677PALSa in the proper targeting of growth factor receptors to the basolateral surface of epithelial cells. A close homologue of sbg533677PALSa is the mouse protein, Pals. Pals represents a new subfamily of membrane-associated guanylate kinases that allow for multiple targeting complexes containing mLin-7 that is necessary for the proper targeting of the Let-23 growth factor receptor to the basolateral surface of epithelial cells (Kamberov E, Makarova O, Roh M, Liu A, Karnak D, Straight S, Margolis B Molecular cloning and characterization of Pals, proteins associated with mLin-7. J Biol Chem 2000 Apr 14; 275(15):11425-31).	Cancer, infection, autoimmune disorders, wound healing disorders and hematopoietic disorders
sbg535067 MELAa	An embodiment of the invention is the use of sbg535067MELAa in detection, treatment and prevention of cancers, e.g. melanoma. A close homologue of sbg535067MELAa is a human melanoma-associated antigen. Human melanoma-associated antigen may be useful in detection, treatment and prevention of cancers. (Pavitt R. dJ142F18.1 similar to melanoma-associated antigen. Accession no. CAA19928, Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridge shire, CB10 1SA, UK)	Melanoma
sbg590979 THP	An embodiment of the invention is the use of sbg590979THP in regulating cytokine circulation. A close homologue of sbg590979THP is a Human Tamm-Horsfall Protein. Human Tamm-Horsfall Protein, a major urinary protein, is linked to membranes via a glycosylphosphatidylinositol (GPI) anchor, and mainly exists at the luminal face of cells of the thick ascending limb of Henle's loop (TAL) and early distal convoluted tubules of nephron. A portion of the Tamm-Horsfall protein is cleaved by the action of proteases, and subsequently is secreted in urine. Since the urinary Tamm-Horsfall protein has a high gel-forming tendency, it has been postulated that it takes part in the water impermeability of TAL. It is also proposed that the Tamm-Horsfall protein may inhibit the colonization of pathogens in the renal mucosa in that the soluble form competes with that exposed at the plasma membrane (Pressac M; 2000; Ann Biol Clin (Paris) 58:167-76)	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, diabetic nephropathy, and nephrolithiasis
sbg658629 CRF	An embodiment of the invention is the use of sbg658629CRF in regulating central nervous system functions, e.g. motor functions. A close homologue of sbg658629CRF is C1q. C1q is a subunit of the C1 enzyme complex that activates the serum complement system. It has been shown that human CRF transcript is expressed at highest levels in the brain, particularly in the brainstem. Similarly, in mouse brain CRF transcripts are most abundant in areas of the nervous system involved in motor function (Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR, and Pereira-Smith OM.; 1999, Brain Res. Mol. Brain Res. 63:233-240).	Nervous system disorder

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg507131 mannosidase	An embodiment of the invention is the use of sbg507131mannosidase in cell-cell and cell-substratum interactions affecting processes such as lymphocyte trafficking, immune cell stimulation, embryogenesis, and cancer metastasis. A close homologue of sbg507131mannosidase is Alpha-D-mannosidase. Alpha-D-mannosidase is involved in the catabolism of glycoproteins through the sequential degradation of mannose and complex oligosaccharides. Specific carbohydrate structures are involved in cell-cell and cell-substratum interactions affecting processes such as lymphocyte trafficking, immune cell stimulation, embryogenesis, and cancer metastasis. Therefore, alpha-mannosidase inhibitors have been selected as anticancer agents for clinical tests (Goss PE, Baker MA, Carver JP, Dennis JW; 1995; Clin Cancer Res 1:935-44). Besides, in the human alpha-mannosidosis is an autosomal recessive lysosomal storage disease caused by the deficiency of lysosomal alpha-D-mannosidase activity (Beccari T, Stinchi S, Orlacchio A; 1999; Biosci Rep 19:157-62).	Cancer , infection,  autoimmune disorder,  hematopoietic disorder,  wound healing disorders,  inflammation,  and aplha- mannosidosis
sbg655871 calgizzarin- like	An embodiment of the invention is the use of sbg655871calgizzarin-like in the regulation of cell transformation and/or differentiation. A close homologue of sbg655871calgizzarin-like is human calgizzarin. The expression of human calgizzarin was remarkably elevated in colorectal cancers (Tanaka M, Adzuma K, Iwami M, Yoshimoto K, Monden Y, Itakura. 1995 Cancer. Lett 89:195-200 ). In addition, it has been reported that calgizzarin, or MLN70, is one of several genes expressed in breast cancer-derived metastatic axillary lymph nodes but not in normal lymph nodes or breast fibroadenomas (Tomasetto C, Regnier C, Moog-Lutz C, Mattei MG, Chenard MP, Lidereau R, Basset P, Rio MC. 1995. Genomics 28:367-76). It is becoming clear that calgizzarin-related proteins may be involved in the regulation of cell transformation and/or differentiation (Moog-Lutz C, Bouillet P, Regnier CH, Tomasetto C, Mattei MG, Chenard MP, Anglard P, Rio MC, Basset P. 1995. Int J Cancer 63:297-303).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg506454 MPG-1	An embodiment of the invention is the use of sbg506454MPG-1 in regulating the immune system and familial hemophagocytic lymphohistiocytosis. Close homologues of sbg506454MPG-1 are human mpg-1 and perforin. It was shown that the mpg-1 gene may be specifically expressed in macrophages, and it shares a distant ancestry to perforin, a lytic protein found in cytotoxic T lymphocytes and natural killer cells (Spilsbury K, O'Mara MA, Wu WM, Rowe PB, Symonds G, Takayama Y. 1995. Blood 85:1620-9). Analyses of mice deficient in perforin demonstrate that cytotoxicity is critical for immunity against some infections (Harty JT, Tvinnereim AR, White DW. 2000. Annu Rev Immunol 18:275-30). Mutations in the perforin gene were recently identified in familial hemophagocytic lymphohistiocytosis, a fatal disease of early childhood (Fadeel B, Henter JJ, Orrenius S. 2000. Lakartidningen 97:1395-400)	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg659837 OBCAM	An embodiment of the invention is the use of sbg659837OBCAM in cell recognition and adhesion. Close homologues of sbg659837OBCAM are opoid-binding proteins. The opoid-binding protein binds opoid alkaloids in the presence of acidic lipids. It has been shown that the opoid-binding protein shares structural homology with members of the immunoglobulin protein superfamily, most notably with cell-adhesion molecules, such as neural cell adhesion molecules (NCAM) and myelin associated glycoproteins (MAG) (Schofield PR, McFarland KC, Hayflick JS, Wilcox JN, Cho TM, Roy S, Lee NM, Loh HH, Seeburg PH. 1989. EMBO J 8:489-95). It has been shown that opoids can modulate cell-cell interactions of monocytes, and support for links between opoids and the immune system (Loh HH, Smith AP.1990; Annu Rev Pharmacol Toxicol 30:123-47).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg467870 CBP	An embodiment of the invention is the use of sbg467870CBP in tumor cell invasiveness. A close homologue of sbg467870CBP is reticulocalbin. Reticulocalbin is a calcium-binding protein located in the lumen of the ER. The protein contains six conserved regions with similarity to a high affinity calcium-binding motif, the EF-hand (Ozawa M, Muramatsu T. 1993. J Biol Chem 268:699-705). It has been shown that reticulocalbin was overexpressed in highly invasive breast cancer cell lines, but not in poorly invasive ones (Liu Z, Brattain MG, Appert H. 1997. Biochem Biophys Res Commun 231:283-9).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg514112 RNase	An embodiment of the invention is the use of sbg514112RNase as a tool for anticancer therapy and the antagonist of this RNase may be useful in treating apoptosis-related disorders. A close homologue of sbg514112RNase is human keratinocyte-derived RNase-like protein (AAY44192). It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein was thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg962274 FGF-BP	<p>An embodiment of the invention is the use of sbg962274FGF-BP as a modulator of FGF in FGF-responsive cells and/or detection, treatment and prevention of cancers. A close homologue of sbg962274FGF-BP is mouse fibroblast growth factor binding protein 1 (gi:7106317). Murine FGF-BP binds to FGF-2 and can function as a modulator of FGF in FGF-responsive cells. FGF-BP mRNA expression in the adult skin was dramatically increased during early stages of carcinogen-induced transformation in vivo and by ras-activation (Kurtz A, Wang HL, Darwiche N, Harris V, Wellstein A. 1997. Oncogene Jun 5;14(22):2671-81). The induction of the angiogenic modulator FGF-BP by epidermal growth factor was mediated through both MEK/ERK and p38 signal transduction pathways (Harris VK, Coticchia CM, Kagan BL, Ahmad S, Wellstein A, Riegel AT. 2000. J Biol Chem Apr 14;275(15):10802-11). Further more, the FGF-BP was upregulated in carcinogen-induced skin tumors, in squamous cell carcinoma (SCC) and in some colon cancer cell lines and tumor samples (Harris VK, Coticchia CM, List HJ, Wellstein A, Riegel AT. 2000. J Biol Chem Jun 27). Finally, human tumors can utilize FGF-BP as an angiogenic switch molecule, the growth and angiogenesis of xenograft tumors in mice was decreased in parallel with the reduction of FGF-BP. These results indicate the role of FGF-BP in tumor metastases (Czubayko F, Liaudet-Coopman ED, Aigner A, Tuveson AT, Berchem GJ, Wellstein A. 1997. Med. Oct;3(10):1137-40., Jayne DG, Perry SL, Morrison E, Farmery SM, Guillou PJ. 2000. Br J Cancer Mar;82(6):1233-8).</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis and rheumatoid</p>



**Table IV. Quantitative, Tissue-specific mRNA expression detected using SybrMan**

Quantitative, tissue-specific, mRNA expression patterns of the genes were measured using SYBR-Green Quantitative PCR (Applied Biosystems, Foster City, CA; see Schmittgen T.D. et al., Analytical Biochemistry 285:194-204, 2000) and human cDNAs prepared from various human tissues. Gene-specific PCR primers were designed using the first nucleic acid sequence listed in the Sequence List for each gene.

In each gene's first subset table, two replicate measurements of gene of identification (GOI) mRNA were measured from various human tissues (column 2 and 3). The average GOI mRNA copies of the two replicates were made from each tissue RNA (column 4). The average amount of 18S rRNA from each tissue RNA was measured (column 5) and used for normalization. To make each tissue with the same amount of 50 ng of 18S rRNA, the normalization factor (column 6) was calculated by dividing 50 ng with the amount of 18S rRNA measured from each tissue (column 5). The mRNA copies per 50 ng of total RNA were obtained by multiplying each GOI normalization factor and average mRNA copies (column 7).

Fold changes shown in each gene's second subset table were only calculated for disease tissues which have a normal counterpart. There are blanks in the fold change column for all samples that do not have counterparts. In addition, the fold change calculations are the fold change in the disease sample as compared to the normal sample. Accordingly, there will not be a fold change calculation next to any of the normal samples. For patient matched cancer pairs (colon, lung, and breast), each tumor is compared to its specific normal counterpart. When patient-matched normal/disease pairs do not exist, each disease sample was compared back to the average of all the normal samples of that same tissue type. For example, normal brain from the same patient that provided Alzheimer's brain is not applicable. Three normal brain samples and 4 Alzheimer's brain samples are used in the fold change. Three normal samples were averaged, and each of the Alzheimer's samples was compared back to that average.

**Abbreviations**

ALZ Alzheimer's Disease

CT CLONTECH (1020 East Meadow Circle Palo Alto, CA 94303-4230, USA)

KC Sample prepared by GSK investigator

COPD chronic obstructive pulmonary disease

endo endothelial

VEGF vascular endothelial growth factor

bFGF basic fibroblast growth factor

BM bone marrow

osteo osteoblast

OA osteoarthritis

RA rheumatoid arthritis

PBL peripheral blood lymphocytes

PBMNC peripheral blood mononuclear cells

HIV human immunodeficiency virus

HSV Herpes simplex virus

HPV human papilloma virus

Gene Name sbg458463PERLAXINa

Strongly expressed in brain and lung. Overexpressed in lung tumor (1/4). Downregulated in COPD lung. Overexpressed in Alzheimer's disease.

Sample sbg458463PERLAXINa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/5 0 ng total RNA
Subcutaneous Adipocytes Zenbio	41.23	19.93	41.23	3.06	16.34	673.69
Subcutaneous Adipose Zenbio	0.00	3.77	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	8.11	3.36	8.11	0.61	81.97	664.75
Whole Brain Clontech	1249.19	1199.08	1249.19	7.24	6.91	8627.00
Fetal Brain Clontech	4.03	3.17	4.03	0.48	103.95	418.92
Cerebellum Clontech	29.60	2.26	29.60	2.17	23.04	682.03
Cervix	0.00	3.52	0.00	2.42	20.66	0.00
Colon	10.94	11.43	10.94	2.71	18.45	201.85
Endometrium	19.75	10.39	19.75	0.73	68.21	1347.20
Esophagus	3.42	0.00	3.42	1.37	36.50	124.82
Heart Clontech	5.63	8.28	5.63	1.32	37.88	213.26
Hypothalamus	9.61	3.16	9.61	0.32	155.28	1492.24
Ileum	19.50	0.00	19.50	2.58	19.38	377.91
Jejunum	35.72	32.22	35.72	6.60	7.58	270.61
Kidney	6.42	13.66	6.42	2.12	23.58	151.42
Liver	13.55	3.28	13.55	1.50	33.33	451.67
Fetal Liver Clontech	57.57	94.10	57.57	10.40	4.81	276.78
Lung	124.57	127.73	124.57	2.57	19.46	2423.54
Mammary Gland Clontech	60.58	30.84	60.58	13.00	3.85	233.00
Myometrium	6.30	0.00	6.30	2.34	21.37	134.62
Omentum	3.51	7.21	3.51	3.94	12.69	44.54
Ovary	19.14	33.01	19.14	4.34	11.52	220.51
Pancreas	3.28	0.00	3.28	0.81	61.80	202.72
Head of Pancreas	0.00	5.33	0.00	1.57	31.85	0.00
Parotid Gland	17.05	0.00	17.05	5.48	9.12	155.57
Placenta Clontech	36.77	12.63	36.77	5.26	9.51	349.52
Prostate	4.30	18.25	4.30	3.00	16.67	71.67
Rectum	2.68	22.55	2.68	1.23	40.65	108.94
Salivary Gland Clontech	21.54	10.89	21.54	7.31	6.84	147.33
Skeletal Muscle Clontech	0.00	0.00	0.00	1.26	39.68	0.00
Skin	3.35	0.00	3.35	1.21	41.32	138.43
Small Intestine Clontech	0.00	0.00	0.00	0.98	51.07	0.00
Spleen	4.87	0.00	4.87	4.92	10.16	49.49
Stomach	12.63	21.35	12.63	2.73	18.32	231.32
Testis Clontech	0.00	0.00	0.00	0.57	87.87	0.00
Thymus Clontech	45.02	58.50	45.02	9.89	5.06	227.60
Thyroid	19.37	58.11	19.37	2.77	18.05	349.64
Trachea Clontech	24.52	32.52	24.52	9.71	5.15	126.26
Urinary Bladder	17.48	18.43	17.48	5.47	9.14	159.78
Uterus	27.02	14.43	27.02	5.34	9.36	253.00

Sample sbg458463PERLAXINa	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	253.9	507.80	colon normal	
colon tumor GW98-166	21940	228.99	457.98	colon tumor	-1.108782043
colon normal GW98-178	22080	149.04	298.08	colon normal	
colon tumor GW98-177	22060	68.84	137.68	colon tumor	-2.165020337
colon normal GW98-561	23514	61.93	123.86	colon normal	
colon tumor GW98-560	23513	167.95	335.90	colon tumor	2.711932827
colon normal GW98-894	24691	160.94	321.88	colon normal	
colon tumor GW98-893	24690	157.68	315.36	colon tumor	-1.020674784
lung normal GW98-3	20742	4197.38	8394.76	lung normal	
lung tumor GW98-2	20741	176.65	353.30	lung tumor	-23.76099632
lung normal GW97-179	20677	385.26	770.52	lung normal	
lung tumor GW97-178	20676	480.07	960.14	lung tumor	1.246093547
lung normal GW98-165	21922	5999.5	11999.00	lung normal	
lung tumor GW98-164	21921	856.89	1713.78	lung tumor	-7.001482104
lung normal GW98-282	22584	377.61	755.22	lung normal	
lung tumor GW98-281	22583	2559.29	5118.58	lung tumor	6.777601229
breast normal GW00-392	28750	408.18	408.18	breast normal	
breast tumor GW00-391	28746	394.46	788.92	breast tumor	1.932774756
breast normal GW00-413	28798	74.3	74.30	breast normal	
breast tumor GW00-412	28797	258.3	516.60	breast tumor	6.952893674
breast normal GW00-235:238	27592-95	51.75	51.75	breast normal	
breast tumor GW00-231:234	27588-91	238.94	238.94	breast tumor	4.617198068
breast normal GW98-621	23656	556.61	1113.22	breast normal	
breast tumor GW98-620	23655	375.74	751.48	breast tumor	-1.481370096
brain normal BB99-542	25507	94588.67	189177.34	brain normal	
brain normal BB99-406	25509	639.74	1279.48	brain normal	
brain normal BB99-904	25546	230.79	461.58	brain normal	
brain stage 5 ALZ BB99-874	25502	1238.35	2476.70	brain stage 5 ALZ	-25.69526655
brain stage 5 ALZ BB99-887	25503	1317.43	2634.86	brain stage 5 ALZ	-24.15288352
brain stage 5 ALZ BB99-862	25504	1028.9	2057.80	brain stage 5 ALZ	-30.92597272
brain stage 5 ALZ BB99-927	25542	863.06	1726.12	brain stage 5 ALZ	-36.86850663
CT lung KC	normal	3367.92	6735.84	CT lung	
lung 26 KC	normal	95.04	95.04	lung 26	
lung 27 KC	normal	116.4	116.40	lung 27	
lung 24 KC	COPD	44.2	44.20	lung 24	-39.76391403
lung 28 KC	COPD	15.38	15.38	lung 28	-114.2760078
lung 23 KC	COPD	23.06	23.06	lung 23	-76.2170425
lung 25 KC	COPD	82.98	82.98	lung 25	
asthmatic lung ODO3112	29321	2034.33	2034.33	asthmatic lung	1.157470705
asthmatic lung ODO3433	29323	3155.21	6310.42	asthmatic lung	3.590433355

asthmatic lung ODO3397	29322	6352.76	12705.52	asthmatic lung	7.229047005
asthmatic lung ODO4928	29325	2424.25	4848.50	asthmatic lung	2.758646195
endo cells KC	control	41.66	41.66	endo cells	
endo VEGF KC		51.2	51.20	endo VEGF	1.228996639
endo bFGF KC		45.7	45.70	endo bFGF	1.096975516
heart Clontech	normal	63.06	126.12	heart	
heart ( T-1 ) ischemic	29417	479.42	958.84	heart T-1	7.602600698
heart (T-14) non- obstructive DCM	29422	410.97	821.94	heart T-14	6.517126546
heart (T-3399) DCM	29426	486.59	973.18	heart T-3399	7.716301935
adenoid GW99-269	26162	100.09	200.18	adenoid	
tonsil GW98-280	22582	260.2	520.40	tonsil	
T cells PC00314	28453	257.22	514.44	T cells	
PBMNC KC		26.27	26.27	PBMNC	
monocyte KC		33.09	66.18	monocyte	
B cells PC00665	28455	144.41	288.82	B cells	
dendritic cells 28441		159.67	319.34	dendritic cells	
neutrophils	28440	444.77	444.77	neutrophils	
eosinophils	28446	23.29	46.58	eosinophils	
BM unstim KC		9.26	9.26	BM unstim	
BM stim KC		67.52	67.52	BM stim	7.291576674
osteo dif KC		50.27	50.27	osteo dif	
osteo undif KC		9.8	9.80	osteo undif	-5.129591837
chondrocytes		275.5	688.75	chondrocytes	
OA Synovium IP12/01	29462	432.44	432.44	OA Synovium	
OA Synovium NP10/01	29461	315.85	631.70	OA Synovium	
OA Synovium NP57/00	28464	397.41	794.82	OA Synovium	
RA Synovium NP03/01	28466	342.52	685.04	RA Synovium	
RA Synovium NP71/00	28467	439.34	878.68	RA Synovium	
RA Synovium NP45/00	28475	222.07	444.14	RA Synovium	
OA bone (biobank)	29217	152.61	152.61	OA bone (biobank)	
OA bone Sample 1	J. Emory	623.73	1247.46	OA bone	
OA bone Sample 2	J. Emory	330.6	661.20	OA bone	
Cartilage (pool)	Normal	592.05	1184.10	Cartilage (pool)	
Cartilage (pool)	OA	204.82	409.64	Cartilage (pool)	-2.890586857
PBL uninfected	28441	488.95	977.90	PBL uninfected	
PBL HIV IIIB	28442	261.88	523.76	PBL HIV IIIB	-1.867076524
MRC5 uninfected (100%)	29158	476.47	952.94	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	216.34	432.68	MRC5 HSV strain F	-2.202412869
W12 cells	29179	182.76	365.52	W12 cells	
Keratinocytes	29180	124.58	249.16	Keratinocytes	

Gene Name sbg458463PERLAXINa

Disease tissues	Fold Change in Disease
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	Population Relative to Normal
colon tumor	-1.11
colon tumor	-2.17
colon tumor	2.71
colon tumor	-1.02
lung tumor	-23.76
lung tumor	1.25
lung tumor	-7.00
lung tumor	6.78
breast tumor	1.93
breast tumor	6.95
breast tumor	4.62
breast tumor	-1.48
brain stage 5 ALZ	-25.70
brain stage 5 ALZ	-24.15
brain stage 5 ALZ	-30.93
brain stage 5 ALZ	-36.87
lung 24	-39.76
lung 28	-114.28
lung 23	-76.22
asthmatic lung	1.16
asthmatic lung	3.59
asthmatic lung	7.23
asthmatic lung	2.76
endo VEGF	1.23
endo bFGF	1.10
heart T-1	7.60
heart T-14	6.52
heart T-3399	7.72
BM stim	7.29
osteo undif	-5.13
Cartilage (pool)	-2.89
PBL HIV IIIB	-1.87
MRC5 HSV strain F	-2.20

Gene Name sbg507885RDPa and sbg507885RDPb

Strongly expressed in immune cells. Corroborating expression in OA and RA samples suggesting a role in this disease. Expression in brain outside of cortex, cerebellum, and hypothalamus indicating localized expression in brain.

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Sample sbg507885RDPa and sbg507885RDPb	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0.44	0.00	0.22	3.06	16.34	3.59
Subcutaneous Adipose Zenbio	0.00	1.46	0.73	0.96	52.36	38.22
Adrenal Gland Clontech	2.56	1.63	2.10	0.61	81.97	171.72

Whole Brain Clontech	354.41	170.16	262.29	7.24	6.91	1811.36
Fetal Brain Clontech	1.81	1.98	1.90	0.48	103.95	196.99
Cerebellum Clontech	1.42	4.83	3.13	2.17	23.04	72.00
Cervix	1.00	0.94	0.97	2.42	20.66	20.04
Colon	7.32	3.78	5.55	2.71	18.45	102.40
Endometrium	6.52	0.99	3.76	0.73	68.21	256.14
Esophagus	1.30	0.65	0.98	1.37	36.50	35.58
Heart Clontech	0.45	1.81	1.13	1.32	37.88	42.80
Hypothalamus	0.00	0.00	0.00	0.32	155.28	0.00
Ileum	14.77	2.05	8.41	2.58	19.38	162.98
Jejunum	12.85	18.38	15.62	6.60	7.58	118.30
Kidney	0.71	0.70	0.71	2.12	23.58	16.63
Liver	0.84	14.92	7.88	1.50	33.33	262.67
Fetal Liver Clontech	34.52	48.23	41.38	10.40	4.81	198.92
Lung	0.00	6.12	3.06	2.57	19.46	59.53
Mammary Gland Clontech	6.69	1.13	3.91	13.00	3.85	15.04
Myometrium	0.00	0.00	0.00	2.34	21.37	0.00
Omentum	19.39	22.18	20.79	3.94	12.69	263.77
Ovary	10.10	8.28	9.19	4.34	11.52	105.88
Pancreas	0.62	0.75	0.69	0.81	61.80	42.34
Head of Pancreas	0.51	0.80	0.66	1.57	31.85	20.86
Parotid Gland	0.79	12.98	6.89	5.48	9.12	62.82
Placenta Clontech	5.82	6.21	6.02	5.26	9.51	57.18
Prostate	0.94	0.00	0.47	3.00	16.67	7.83
Rectum	9.47	0.59	5.03	1.23	40.65	204.47
Salivary Gland Clontech	1.06	4.83	2.95	7.31	6.84	20.14
Skeletal Muscle Clontech	0.89	0.00	0.45	1.26	39.68	17.66
Skin	0.70	0.92	0.81	1.21	41.32	33.47
Small Intestine Clontech	2.38	0.00	1.19	0.98	51.07	60.78
Spleen	5.42	0.63	3.03	4.92	10.16	30.74
Stomach	0.00	14.37	7.19	2.73	18.32	131.59
Testis Clontech	29.69	16.00	22.85	0.57	87.87	2007.47
Thymus Clontech	27.94	42.80	35.37	9.89	5.06	178.82
Thyroid	0.00	5.97	2.99	2.77	18.05	53.88
Trachea Clontech	35.39	143.02	89.21	9.71	5.15	459.35
Urinary Bladder	0.56	0.00	0.28	5.47	9.14	2.56
Uterus	6.57	32.58	19.58	5.34	9.36	183.29

Sample sbg507885RDPa and sbg507885RDPb	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	45.66	91.32	colon normal	
colon tumor GW98-166	21940	43.18	86.36	colon tumor	-1.057433997
colon normal GW98-178	22080	20.11	40.22	colon normal	
colon tumor GW98-177	22060	10.96	21.92	colon tumor	-1.834854015
colon normal GW98-561	23514	31.65	63.30	colon normal	
colon tumor GW98-560	23513	17.32	34.64	colon tumor	-1.827367206
colon normal GW98-894	24691	47.87	95.74	colon normal	

colon tumor GW98-893	24690	19.49	38.98	colon tumor	-2.456131349
lung normal GW98-3	20742	92.38	184.76	lung normal	
lung tumor GW98-2	20741	0	0.00	lung tumor	-184.76
lung normal GW97-179	20677	118.63	237.26	lung normal	
lung tumor GW97-178	20676	179.06	358.12	lung tumor	1.509398972
lung normal GW98-165	21922	282.77	565.54	lung normal	
lung tumor GW98-164	21921	127.86	255.72	lung tumor	-2.211559518
lung normal GW98-282	22584	34.81	69.62	lung normal	
lung tumor GW98-281	22583	14.9	29.80	lung tumor	-2.336241611
breast normal GW00-392	28750	19.47	19.47	breast normal	
breast tumor GW00-391	28746	21.61	43.22	breast tumor	2.219825372
breast normal GW00-413	28798	19.77	19.77	breast normal	
breast tumor GW00-412	28797	28.47	56.94	breast tumor	2.880121396
breast normal GW00-235:238	27592-95	8.87	8.87	breast normal	
breast tumor GW00-231:234	27588-91	19.37	19.37	breast tumor	2.183765502
breast normal GW98-621	23656	40.14	80.28	breast normal	
breast tumor GW98-620	23655	8.92	17.84	breast tumor	-4.5
brain normal BB99-542	25507	136.73	273.46	brain normal	
brain normal BB99-406	25509	74.17	148.34	brain normal	
brain normal BB99-904	25546	103.79	207.58	brain normal	
brain stage 5 ALZ BB99-874	25502	15.31	30.62	brain stage 5 ALZ	-6.851513172
brain stage 5 ALZ BB99-887	25503	256.01	512.02	brain stage 5 ALZ	2.440592329
brain stage 5 ALZ BB99-862	25504	75.06	150.12	brain stage 5 ALZ	-1.397504219
brain stage 5 ALZ BB99-927	25542	142.17	284.34	brain stage 5 ALZ	1.355333821
CT lung KC	normal	51.66	103.32	CT lung	
lung 26 KC	normal	25.26	25.26	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	8.84	8.84	lung 24	-4.022624434
lung 28 KC	COPD	2.6	2.60	lung 28	-13.67692308
lung 23 KC	COPD	5.92	5.92	lung 23	-6.006756757
lung 25 KC	COPD	13.66	13.66	lung 25	
asthmatic lung ODO3112	29321	22.47	22.47	asthmatic lung	-1.582554517
asthmatic lung ODO3433	29323	72.48	144.96	asthmatic lung	4.076490439
asthmatic lung ODO3397	29322	89.06	178.12	asthmatic lung	5.008998875
asthmatic lung ODO4928	29325	165.77	331.54	asthmatic lung	9.323397075
endo cells KC	control	3.74	3.74	endo cells	
endo VEGF KC		0	0.00	endo VEGF	-3.74
endo bFGF KC		0	0.00	endo bFGF	-3.74
heart Clontech	normal	44.05	88.10	heart	
heart (T-1) ischemic	29417	34.71	69.42	heart T-1	-1.269086719
heart (T-14) non-obstructive DCM	29422	6.78	13.56	heart T-14	-6.497050147
heart (T-3399) DCM	29426	13.42	26.84	heart T-3399	-3.282414307
adenoid GW99-269	26162	79.2	158.40	adenoid	
tonsil GW98-280	22582	92.31	184.62	tonsil	
T cells PC00314	28453	499.1	998.20	T cells	
PBMNC KC		16.17	16.17	PBMNC	
monocyte KC		8.33	16.66	monocyte	

B cells PC00665	28455	1260.77	2521.54	B cells	
dendritic cells 28441		153.63	307.26	dendritic cells	
neutrophils	28440	5938.24	5938.24	neutrophils	
eosinophils	28446	1471.53	2943.06	eosinophils	
BM unstim KC		9.62	9.62	BM unstim	
BM stim KC		31.23	31.23	BM stim	3.246361746
osteo dif KC		0	0.00	osteo dif	
osteo undif KC		0	0.00	osteo undif	0
chondrocytes		0.68	1.70	chondrocytes	
OA Synovium IP12/01	29462	80.64	80.64	OA Synovium	
OA Synovium NP10/01	29461	121	242.00	OA Synovium	
OA Synovium NP57/00	28464	117.75	235.50	OA Synovium	
RA Synovium NP03/01	28466	189.18	378.36	RA Synovium	
RA Synovium NP71/00	28467	313.76	627.52	RA Synovium	
RA Synovium NP45/00	28475	146.34	292.68	RA Synovium	
OA bone (biobank)	29217	171.21	171.21	OA bone (biobank)	
OA bone Sample 1	J. Emory	71.91	143.82	OA bone	
OA bone Sample 2	J. Emory	132.79	265.58	OA bone	
Cartilage (pool)	Normal	19.06	38.12	Cartilage (pool)	
Cartilage (pool)	OA	31.65	63.30	Cartilage (pool)	1.660545645
PBL uninfected	28441	99.28	198.56	PBL uninfected	
PBL HIV IIIB	28442	57.94	115.88	PBL HIV IIIB	-1.713496721
MRC5 uninfected (100%)	29158	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	206.39	412.78	MRC5 HSV strain F	412.78
W12 cells	29179	0	0.00	W12 cells	
Keratinocytes	29180	4.35	8.70	Keratinocytes	

Gene Name sbg507885RDPa and sbg507885RDPb

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.06
colon tumor	-1.83
colon tumor	-1.83
colon tumor	-2.46
lung tumor	-184.76
lung tumor	1.51
lung tumor	-2.21
lung tumor	-2.34
breast tumor	2.22
breast tumor	2.88
breast tumor	2.18
breast tumor	-4.50
brain stage 5 ALZ	-6.85
brain stage 5 ALZ	2.44
brain stage 5 ALZ	-1.40
brain stage 5 ALZ	1.36
lung 24	-4.02



lung 28	-13.68
lung 23	-6.01
asthmatic lung	-1.58
asthmatic lung	4.08
asthmatic lung	5.01
asthmatic lung	9.32
endo VEGF	-3.74
endo bFGF	-3.74
heart T-1	-1.27
heart T-14	-6.50
heart T-3399	-3.28
BM stim	3.25
osteo undif	0.00
Cartilage (pool)	1.66
PBL HIV IIIB	-1.71
MRC5 HSV strain F	412.78

**Gene Name SBh511364.NR-CAMa and SBh511364.NR-CAMb**

Strongly expressed in synovium. Specific expression profile and lack of corroborating expression in immune cells indicates that this expression may be derived from synoviocytes. Strongly expressed in brain and to a lesser degree, hypothalamus. Low expression in cortex.

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Sample SBh511364.NR- CAMa and SBh511364.NR- CAMb	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	8.81	15.21	12.01	3.06	16.34	196.24
Subcutaneous Adipose Zenbio	0.65	0.60	0.63	0.96	52.36	32.72
Adrenal Gland Clontech	5.82	2.88	4.35	0.61	81.97	356.56
Whole Brain Clontech	745.46	885.20	815.33	7.24	6.91	5630.73
Fetal Brain Clontech	2.54	7.10	4.82	0.48	103.95	501.04
Cerebellum Clontech	2.00	1.60	1.80	2.17	23.04	41.47
Cervix	5.24	5.57	5.41	2.42	20.66	111.67
Colon	19.12	9.91	14.52	2.71	18.45	267.80
Endometrium	5.89	3.09	4.49	0.73	68.21	306.28
Esophagus	3.36	5.73	4.55	1.37	36.50	165.88
Heart Clontech	11.19	4.50	7.85	1.32	37.88	297.16
Hypothalamus	6.23	9.33	7.78	0.32	155.28	1208.07
Ileum	22.13	14.54	18.34	2.58	19.38	355.33
Jejunum	43.08	28.67	35.88	6.60	7.58	271.78
Kidney	6.61	2.38	4.50	2.12	23.58	106.01
Liver	5.71	7.80	6.76	1.50	33.33	225.17
Fetal Liver Clontech	58.58	39.22	48.90	10.40	4.81	235.10
Lung	21.54	14.27	17.91	2.57	19.46	348.35
Mammary Gland Clontech	74.10	70.13	72.12	13.00	3.85	277.37
Myometrium	14.20	14.00	14.10	2.34	21.37	301.28
Omentum	10.02	8.87	9.45	3.94	12.69	119.86

Ovary	18.13	21.78	19.96	4.34	11.52	229.90
Pancreas	5.35	5.01	5.18	0.81	61.80	320.15
Head of Pancreas	15.48	17.71	16.60	1.57	31.85	528.50
Parotid Gland	15.65	18.09	16.87	5.48	9.12	153.92
Placenta Clontech	39.73	32.58	36.16	5.26	9.51	343.68
Prostate	11.18	10.70	10.94	3.00	16.67	182.33
Rectum	13.03	18.25	15.64	1.23	40.65	635.77
Salivary Gland Clontech	45.23	37.40	41.32	7.31	6.84	282.59
Skin	13.36	18.71	16.04	1.21	41.32	662.60
Small Intestine Clontech	9.35	14.90	12.13	0.98	51.07	619.25
Spleen	20.53	16.75	18.64	4.92	10.16	189.43
Stomach	10.15	11.21	10.68	2.73	18.32	195.60
Testis Clontech	4.21	9.04	6.63	0.57	87.87	582.16
Thymus Clontech	107.54	69.67	88.61	9.89	5.06	447.95
Thyroid	16.42	20.77	18.60	2.77	18.05	335.65
Trachea Clontech	45.92	41.96	43.94	9.71	5.15	226.26
Urinary Bladder	32.67	27.42	30.05	5.47	9.14	274.63
Uterus	16.56	13.13	14.85	5.34	9.36	139.00

Sample SBh511364.NR-CAMa and SBh511364.NR-CAMb	Reg number (GSK identifier )	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	341.84	683.68	colon normal	
colon tumor GW98-166	21940	698.49	1396.98	colon tumor	2.043324362
colon normal GW98-178	22080	173.88	347.76	colon normal	
colon tumor GW98-177	22060	69.79	139.58	colon tumor	-2.491474423
colon normal GW98-561	23514	131.42	262.84	colon normal	
colon tumor GW98-560	23513	89.43	178.86	colon tumor	-1.469529241
colon normal GW98-894	24691	182.2	364.40	colon normal	
colon tumor GW98-893	24690	119.24	238.48	colon tumor	-1.528010735
lung normal GW98-3	20742	366.92	733.84	lung normal	
lung tumor GW98-2	20741	171.96	343.92	lung tumor	-2.133752035
lung normal GW97-179	20677	779.87	1559.74	lung normal	
lung tumor GW97-178	20676	276.89	553.78	lung tumor	-2.816533642
lung normal GW98-165	21922	325.67	651.34	lung normal	
lung tumor GW98-164	21921	1297.39	2594.78	lung tumor	3.983756563
lung normal GW98-282	22584	608.41	1216.82	lung normal	
lung tumor GW98-281	22583	164.45	328.90	lung tumor	-3.699665552
breast normal GW00-392	28750	138.27	138.27	breast normal	
breast tumor GW00-391	28746	181.83	363.66	breast tumor	2.630071599
breast normal GW00-413	28798	38.99	38.99	breast normal	
breast tumor GW00-412	28797	90.26	180.52	breast tumor	4.629905104
breast normal GW00-235:238	27592-95	34.69	34.69	breast normal	
breast tumor GW00-231:234	27588-91	189.47	189.47	breast tumor	5.461804555
breast normal GW98-621	23656	375.65	751.30	breast normal	
breast tumor GW98-620	23655	165.82	331.64	breast tumor	-2.265408274
brain normal BB99-542	25507	193.78	387.56	brain normal	
brain normal BB99-406	25509	90.91	181.82	brain normal	

brain normal BB99-904	25546	106.82	213.64	brain normal	
brain stage 5 ALZ BB99-874	25502	107.53	215.06	brain stage 5 ALZ	-1.213645804
brain stage 5 ALZ BB99-887	25503	178.51	357.02	brain stage 5 ALZ	1.367857781
brain stage 5 ALZ BB99-862	25504	134.36	268.72	brain stage 5 ALZ	1.029552246
brain stage 5 ALZ BB99-927	25542	99.03	198.06	brain stage 5 ALZ	-1.31781615
CT lung KC	normal	260.82	521.64	CT lung	
lung 26 KC	normal	5.72	5.72	lung 26	
lung 27 KC	normal	1.05	1.05	lung 27	
lung 24 KC	COPD	2.04	2.04	lung 24	-64.84803922
lung 28 KC	COPD	2.13	2.13	lung 28	-62.10798122
lung 23 KC	COPD	5.32	5.32	lung 23	-24.86654135
lung 25 KC	COPD	0.75	0.75	lung 25	
asthmatic lung ODO3112	29321	153.45	153.45	asthmatic lung	1.159951621
asthmatic lung ODO3433	29323	324.42	648.84	asthmatic lung	4.904679114
asthmatic lung ODO3397	29322	940.06	1880.12	asthmatic lung	14.21210976
asthmatic lung ODO4928	29325	336.17	672.34	asthmatic lung	5.082319147
endo cells KC	control	17.87	17.87	endo cells	
endo VEGF KC		3.69	3.69	endo VEGF	-4.842818428
endo bFGF KC		1.99	1.99	endo bFGF	-8.979899497
heart Clontech	normal	103.46	206.92	heart	
heart (T-1) ischemic	29417	82.96	165.92	heart T-1	-1.24710704
heart (T-14) non-obstructive DCM	29422	95.28	190.56	heart T-14	-1.085852225
heart (T-3399) DCM	29426	82.5	165.00	heart T-3399	-1.254060606
adenoid GW99-269	26162	194.24	388.48	adenoid	
tonsil GW98-280	22582	229.68	459.36	tonsil	
T cells PC00314	28453	96.61	193.22	T cells	
PBMNC KC		4.33	4.33	PBMNC	
monocyte KC		19.34	38.68	monocyte	
B cells PC00665	28455	87.76	175.52	B cells	
dendritic cells 28441		38.09	76.18	dendritic cells	
neutrophils	28440	37.8	37.80	neutrophils	
eosinophils	28446	55.24	110.48	eosinophils	
BM unstim KC		9.02	9.02	BM unstim	
BM stim KC		5.15	5.15	BM stim	-1.751456311
osteo dif KC		1.36	1.36	osteo dif	
osteo undif KC		1.62	1.62	osteo undif	1.191176471
chondrocytes		15.33	38.33	chondrocytes	
OA Synovium IP12/01	29462	761.5	761.50	OA Synovium	
OA Synovium NP10/01	29461	331.41	662.82	OA Synovium	
OA Synovium NP57/00	28464	1027.35	2054.70	OA Synovium	
RA Synovium NP03/01	28466	1550.08	3100.16	RA Synovium	
RA Synovium NP71/00	28467	1537.93	3075.86	RA Synovium	
RA Synovium NP45/00	28475	2117.45	4234.90	RA Synovium	
OA bone (biobank)	29217	15.14	15.14	OA bone (biobank)	
OA bone Sample 1	J. Emory	147.58	295.16	OA bone	
OA bone Sample 2	J. Emory	78.86	157.72	OA bone	
Cartilage (pool)	Normal	170.3	340.60	Cartilage (pool)	

Cartilage (pool)	OA	107.65	215.30	Cartilage (pool)	-1.581978634
PBL uninfected	28441	23	46.00	PBL uninfected	
PBL HIV IIIB	28442	29.11	58.22	PBL HIV IIIB	1.265652174
MRC5 uninfected (100%)	29158	181.22	362.44	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	37.26	74.52	MRC5 HSV strain F	-4.863660762
W12 cells	29179	92.73	185.46	W12 cells	
Keratinocytes	29180	55.64	111.28	Keratinocytes	

Gene Name SBh511364.NR-CAMa and SBh511364.NR-CAMb

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	2.04
colon tumor	-2.49
colon tumor	-1.47
colon tumor	-1.53
lung tumor	-2.13
lung tumor	-2.82
lung tumor	3.98
lung tumor	-3.70
breast tumor	2.63
breast tumor	4.63
breast tumor	5.46
breast tumor	-2.27
brain stage 5 ALZ	-1.21
brain stage 5 ALZ	1.37
brain stage 5 ALZ	1.03
brain stage 5 ALZ	-1.32
lung 24	-64.85
lung 28	-62.11
lung 23	-24.87
asthmatic lung	1.16
asthmatic lung	4.90
asthmatic lung	14.21
asthmatic lung	5.08
endo VEGF	-4.84
endo bFGF	-8.98
heart T-1	-1.25
heart T-14	-1.09
heart T-3399	-1.25
BM stim	-1.75
osteo undif	1.19
Cartilage (pool)	-1.58
PBL HIV IIIB	1.27
MRC5 HSV strain F	-4.86

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Gene Name SBh511827.C1q-related factor

Expression in T and B cells. Corroborating expression in OA and RA samples suggesting role in this disease. Expression in tumors may be due to infiltration of immune cells. High brain expression in whole brain and cortex but does not correlate with Alzheimer's disease.

Sample SBh511827.C1q- related factor	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	10.01	5.60	7.81	3.06	16.34	127.53
Subcutaneous Adipose Zenbio	0.00	2.57	1.29	0.96	52.36	67.28
Adrenal Gland Clontech	0.00	0.00	0.00	0.61	81.97	0.00
Whole Brain Clontech	5567.93	8662.87	7115.40	7.24	6.91	49139.50
Fetal Brain Clontech	0.00	2.90	1.45	0.48	103.95	150.73
Cerebellum Clontech	16.42	20.36	18.39	2.17	23.04	423.73
Cervix	7.42	5.99	6.71	2.42	20.66	138.53
Colon	48.72	28.04	38.38	2.71	18.45	708.12
Endometrium	2.79	0.00	1.40	0.73	68.21	95.16
Esophagus	0.00	0.00	0.00	1.37	36.50	0.00
Heart Clontech	6.47	0.00	3.24	1.32	37.88	122.54
Hypothalamus	0.66	0.00	0.33	0.32	155.28	51.24
Ileum	93.23	38.67	65.95	2.58	19.38	1278.10
Jejunum	139.58	66.22	102.90	6.60	7.58	779.55
Kidney	3.44	1.90	2.67	2.12	23.58	62.97
Liver	5.92	2.25	4.09	1.50	33.33	136.17
Fetal Liver Clontech	660.71	619.22	639.97	10.40	4.81	3076.75
Lung	8.32	30.50	19.41	2.57	19.46	377.63
Mammary Gland Clontech	83.57	132.39	107.98	13.00	3.85	415.31
Myometrium	3.80	7.92	5.86	2.34	21.37	125.21
Omentum	38.71	144.15	91.43	3.94	12.69	1160.28
Ovary	20.35	30.49	25.42	4.34	11.52	292.86
Pancreas	3.05	6.19	4.62	0.81	61.80	285.54
Head of Pancreas	0.00	0.00	0.00	1.57	31.85	0.00
Parotid Gland	508.91	732.28	620.60	5.48	9.12	5662.36
Placenta Clontech	41.43	20.41	30.92	5.26	9.51	293.92
Prostate	3.11	0.00	1.56	3.00	16.67	25.92
Rectum	32.59	24.20	28.40	1.23	40.65	1154.27
Salivary Gland Clontech	333.69	307.24	320.47	7.31	6.84	2191.96
Skeletal Muscle Clontech	0.00	3.23	1.62	1.26	39.68	64.09
Skin	0.00	0.00	0.00	1.21	41.32	0.00
Small Intestine Clontech	0.00	0.00	0.00	0.98	51.07	0.00
Spleen	6.23	29.09	17.66	4.92	10.16	179.47
Stomach	14.40	28.92	21.66	2.73	18.32	396.70
Testis Clontech	0.00	2.81	1.41	0.57	87.87	123.46
Thymus Clontech	1882.59	1917.19	1899.89	9.89	5.06	9605.11
Thyroid	8.33	5.07	6.70	2.77	18.05	120.94

Trachea Clontech	114.59	259.72	187.16	9.71	5.15	963.72
Urinary Bladder	71.47	89.07	80.27	5.47	9.14	733.73
Uterus	30.66	37.35	34.01	5.34	9.36	318.40

Sample SBh511827.C1q-related factor	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/5 0 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	5744.02	11488.04	colon normal	
colon tumor GW98-166	21940	6292.52	12585.04	colon tumor	1.095490615
colon normal GW98-178	22080	320.97	641.94	colon normal	
colon tumor GW98-177	22060	1579.81	3159.62	colon tumor	4.921986478
colon normal GW98-561	23514	1441.03	2882.06	colon normal	
colon tumor GW98-560	23513	593.17	1186.34	colon tumor	-2.429371007
colon normal GW98-894	24691	3163.53	6327.06	colon normal	
colon tumor GW98-893	24690	1149.98	2299.96	colon tumor	-2.750943495
lung normal GW98-3	20742	3695.92	7391.84	lung normal	
lung tumor GW98-2	20741	731.09	1462.18	lung tumor	-5.055355702
lung normal GW97-179	20677	1378.74	2757.48	lung normal	
lung tumor GW97-178	20676	1448.64	2897.28	lung tumor	1.050698464
lung normal GW98-165	21922	3139.74	6279.48	lung normal	
lung tumor GW98-164	21921	8081.51	16163.02	lung tumor	2.573942428
lung normal GW98-282	22584	1632.83	3265.66	lung normal	
lung tumor GW98-281	22583	764.62	1529.24	lung tumor	-2.135479061
breast normal GW00-392	28750	2333.36	2333.36	breast normal	
breast tumor GW00-391	28746	2670.09	5340.18	breast tumor	2.288622416
breast normal GW00-413	28798	1982.15	1982.15	breast normal	
breast tumor GW00-412	28797	1739.48	3478.96	breast tumor	1.755144666
breast normal GW00-235:238	27592-95	1835.31	1835.31	breast normal	
breast tumor GW00-231:234	27588-91	9829.72	9829.72	breast tumor	5.35589083
breast normal GW98-621	23656	2824.18	5648.36	breast normal	
breast tumor GW98-620	23655	5401.77	10803.54	breast tumor	1.91268616
brain normal BB99-542	25507	4282.26	8564.52	brain normal	
brain normal BB99-406	25509	5101.69	10203.38	brain normal	
brain normal BB99-904	25546	3412.26	6824.52	brain normal	
brain stage 5 ALZ BB99-874	25502	1341.14	2682.28	brain stage 5 ALZ	-3.180431076
brain stage 5 ALZ BB99-887	25503	7475.28	14950.56	brain stage 5 ALZ	1.752537665
brain stage 5 ALZ BB99-862	25504	4871.16	9742.32	brain stage 5 ALZ	1.142016269
brain stage 5 ALZ BB99-927	25542	4972.65	9945.30	brain stage 5 ALZ	1.165810033
CT lung KC	normal	622.18	1244.36	CT lung	
lung 26 KC	normal	1547.5	1547.50	lung 26	
lung 27 KC	normal	8.75	8.75	lung 27	
lung 24 KC	COPD	45	45.00	lung 24	-15.69138889
lung 28 KC	COPD	107.35	107.35	lung 28	-6.577666511
lung 23 KC	COPD	245.33	245.33	lung 23	-2.878215057
lung 25 KC	COPD	23.84	23.84	lung 25	
asthmatic lung ODO3112	29321	518.92	518.92	asthmatic lung	-1.360734795

asthmatic lung ODO3433	29323	893.67	1787.34	asthmatic lung	2.53123971
asthmatic lung ODO3397	29322	2195.27	4390.54	asthmatic lung	6.217904371
asthmatic lung ODO4928	29325	695.54	1391.08	asthmatic lung	1.970054347
endo cells KC	control	16.49	16.49	endo cells	
endo VEGF KC		119.58	119.58	endo VEGF	7.251667677
endo bFGF KC		17.05	17.05	endo bFGF	1.033959976
heart Clontech	normal	166.69	333.38	heart	
heart (T-1 ) ischemic	29417	1046.33	2092.66	heart T-1	6.277101206
heart (T-14) non-obstructive DCM	29422	438.65	877.30	heart T-14	2.631531586
heart (T-3399) DCM	29426	634.06	1268.12	heart T-3399	3.803827464
adenoid GW99-269	26162	285.91	571.82	adenoid	
tonsil GW98-280	22582	912.43	1824.86	tonsil	
T cells PC00314	28453	2710.37	5420.74	T cells	
PBMNC KC		53.93	53.93	PBMNC	
monocyte KC		97.03	194.06	monocyte	
B cells PC00665	28455	2096.55	4193.10	B cells	
dendritic cells 28441		307.67	615.34	dendritic cells	
neutrophils	28440	352.93	352.93	neutrophils	
eosinophils	28446	148.18	296.36	eosinophils	
BM unstim KC		44.62	44.62	BM unstim	
BM stim KC		102.28	102.28	BM stim	2.29224563
osteo dif KC		13.17	13.17	osteo dif	
osteo undif KC		9.04	9.04	osteo undif	-1.456858407
chondrocytes		189.54	473.85	chondrocytes	
OA Synovium IP12/01	29462	9850.71	9850.71	OA Synovium	
OA Synovium NP10/01	29461	4627.57	9255.14	OA Synovium	
OA Synovium NP57/00	28464	3568.61	7137.22	OA Synovium	
RA Synovium NP03/01	28466	4452.77	8905.54	RA Synovium	
RA Synovium NP71/00	28467	4479.74	8959.48	RA Synovium	
RA Synovium NP45/00	28475	10746.73	21493.46	RA Synovium	
OA bone (biobank)	29217	468.68	468.68	OA bone (biobank)	
OA bone Sample 1	J. Emory	2277.5	4555.00	OA bone	
OA bone Sample 2	J. Emory	921.91	1843.82	OA bone	
Cartilage (pool)	Normal	9515.61	19031.22	Cartilage (pool)	
Cartilage (pool)	OA	3862.55	7725.10	Cartilage (pool)	-2.463556459
PBL uninfected	28441	2689.77	5379.54	PBL uninfected	
PBL HIV IIIB	28442	1110.9	2221.80	PBL HIV IIIB	-2.421253038
MRC5 uninfected (100%)	29158	163.61	327.22	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	35.94	71.88	MRC5 HSV strain F	-4.552309405
W12 cells	29179	171.69	343.38	W12 cells	
Keratinocytes	29180	142.68	285.36	Keratinocytes	

Gene Name SBh511827.C1q-related factor

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.10
colon tumor	4.92

colon tumor	-2.43
colon tumor	-2.75
lung tumor	-5.06
lung tumor	1.05
lung tumor	2.57
lung tumor	-2.14
breast tumor	2.29
breast tumor	1.76
breast tumor	5.36
breast tumor	1.91
brain stage 5 ALZ	-3.18
brain stage 5 ALZ	1.75
brain stage 5 ALZ	1.14
brain stage 5 ALZ	1.17
lung 24	-15.69
lung 28	-6.58
lung 23	-2.88
asthmatic lung	-1.36
asthmatic lung	2.53
asthmatic lung	6.22
asthmatic lung	1.97
endo VEGF	7.25
endo bFGF	1.03
heart T-1	6.28
heart T-14	2.63
heart T-3399	3.80
BM stim	2.29
osteo undif	-1.46
Cartilage (pool)	-2.46
PBL HIV IIIB	-2.42
MRC5 HSV strain F	-4.55

**Gene Name** sbg533677PALSa

Expression in immune cells with corroborating expression in asthmatic lung (3/4)

suggesting possible role in Asthma. Overexpressed in heart disease suggesting role in CV

- 5 diseases. Down regulation in HSV infection suggesting possible host cell factor. High brain expression in whole brain and cortex but does not correlate with Alzheimer's disease.

Sample sbg533677PALSa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	51.44	92.64	72.04	3.06	16.34	1177.12
Subcutaneous Adipose Zenbio	5.24	2.42	3.83	0.96	52.36	200.52
Adrenal Gland Clontech	8.53	9.10	8.82	0.61	81.97	722.54
Whole Brain Clontech	15161.45	15339.88	15250.67	7.24	6.91	105322.2 7
Fetal Brain Clontech	18.17	23.22	20.70	0.48	103.95	2151.25
Cerebellum Clontech	219.59	45.25	132.42	2.17	23.04	3051.15



Cervix	122.01	91.28	106.65	2.42	20.66	2203.41
Colon	267.14	172.02	219.58	2.71	18.45	4051.29
Endometrium	18.22	34.03	26.13	0.73	68.21	1782.06
Esophagus	45.23	46.43	45.83	1.37	36.50	1672.63
Heart Clontech	27.22	52.91	40.07	1.32	37.88	1517.61
Hypothalamus	1.28	2.12	1.70	0.32	155.28	263.98
Ileum	94.43	111.58	103.01	2.58	19.38	1996.22
Jejunum	1633.12	2127.36	1880.24	6.60	7.58	14244.24
Kidney	63.84	160.51	112.18	2.12	23.58	2645.64
Liver	29.42	42.03	35.73	1.50	33.33	1190.83
Fetal Liver Clontech	2536.60	2105.61	2321.11	10.40	4.81	11159.16
Lung	136.03	198.77	167.40	2.57	19.46	3256.81
Mammary Gland Clontech	424.73	623.88	524.31	13.00	3.85	2016.56
Myometrium	49.18	119.83	84.51	2.34	21.37	1805.66
Omentum	133.77	211.60	172.69	3.94	12.69	2191.43
Ovary	137.22	102.84	120.03	4.34	11.52	1382.83
Pancreas	24.03	19.46	21.75	0.81	61.80	1343.94
Head of Pancreas	15.98	9.70	12.84	1.57	31.85	408.92
Parotid Gland	164.01	243.65	203.83	5.48	9.12	1859.76
Placenta Clontech	443.13	418.73	430.93	5.26	9.51	4096.29
Prostate	348.78	83.31	216.05	3.00	16.67	3600.75
Rectum	82.65	132.21	107.43	1.23	40.65	4367.07
Salivary Gland Clontech	194.49	469.68	332.09	7.31	6.84	2271.44
Skeletal Muscle Clontech	32.51	69.14	50.83	1.26	39.68	2016.87
Skin	8.94	55.38	32.16	1.21	41.32	1328.93
Small Intestine Clontech	4.50	20.21	12.36	0.98	51.07	631.00
Spleen	115.42	95.13	105.28	4.92	10.16	1069.87
Stomach	58.96	147.19	103.08	2.73	18.32	1887.82
Testis Clontech	28.25	6.42	17.34	0.57	87.87	1523.29
Thymus Clontech	1685.23	1168.51	1426.87	9.89	5.06	7213.70
Thyroid	215.93	210.84	213.39	2.77	18.05	3851.71
Trachea Clontech	195.46	204.92	200.19	9.71	5.15	1030.84
Urinary Bladder	238.82	321.83	280.33	5.47	9.14	2562.39
Uterus	162.57	183.68	173.13	5.34	9.36	1621.02

Sample sbg533677PALSa	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	3216.52	6433.04	colon normal	
colon tumor GW98-166	21940	2713.61	5427.22	colon tumor	-1.185328769
colon normal GW98-178	22080	324.52	649.04	colon normal	
colon tumor GW98-177	22060	657.5	1315.00	colon tumor	2.026069272
colon normal GW98-561	23514	2007.12	4014.24	colon normal	
colon tumor GW98-560	23513	1433.27	2866.54	colon tumor	-1.400378156
colon normal GW98-894	24691	5207.11	10414.22	colon normal	
colon tumor GW98-893	24690	3315.88	6631.76	colon tumor	-1.570355381
lung normal GW98-3	20742	2880.6	5761.20	lung normal	
lung tumor GW98-2	20741	729.25	1458.50	lung tumor	-3.950085704

lung normal GW97-179	20677	2554.17	5108.34	lung normal	
lung tumor GW97-178	20676	3737.04	7474.08	lung tumor	1.463113262
lung normal GW98-165	21922	5054.4	10108.80	lung normal	
lung tumor GW98-164	21921	2226.27	4452.54	lung tumor	-2.270344567
lung normal GW98-282	22584	1861.66	3723.32	lung normal	
lung tumor GW98-281	22583	1654.05	3308.10	lung tumor	-1.125516157
breast normal GW00-392	28750	1333.43	1333.43	breast normal	
breast tumor GW00-391	28746	1994.93	3989.86	breast tumor	2.992178067
breast normal GW00-413	28798	860.05	860.05	breast normal	
breast tumor GW00-412	28797	2402.76	4805.52	breast tumor	5.587489099
breast normal GW00-235:238	27592-95	430.22	430.22	breast normal	
breast tumor GW00-231:234	27588-91	1888.17	1888.17	breast tumor	4.388847566
breast normal GW98-621	23656	3330.56	6661.12	breast normal	
breast tumor GW98-620	23655	1697.99	3395.98	breast tumor	-1.961472093
brain normal BB99-542	25507	11126.07	22252.14	brain normal	
brain normal BB99-406	25509	10597	21194.00	brain normal	
brain normal BB99-904	25546	5508.06	11016.12	brain normal	
brain stage 5 ALZ BB99-874	25502	2411.63	4823.26	brain stage 5 ALZ	-3.763862339
brain stage 5 ALZ BB99-887	25503	10009.75	20019.50	brain stage 5 ALZ	1.102754458
brain stage 5 ALZ BB99-862	25504	6223.93	12447.86	brain stage 5 ALZ	-1.458410254
brain stage 5 ALZ BB99-927	25542	6282.02	12564.04	brain stage 5 ALZ	-1.444924297
CT lung KC	normal	824.22	1648.44	CT lung	
lung 26 KC	normal	460.62	460.62	lung 26	
lung 27 KC	normal	256.02	256.02	lung 27	
lung 24 KC	COPD	218.84	218.84	lung 24	-3.806159751
lung 28 KC	COPD	382.73	382.73	lung 28	-2.176312283
lung 23 KC	COPD	251.06	251.06	lung 23	-3.317692982
lung 25 KC	COPD	966.68	966.68	lung 25	
asthmatic lung ODO3112	29321	1431.16	1431.16	asthmatic lung	1.718202992
asthmatic lung ODO3433	29323	3337.62	6675.24	asthmatic lung	8.014070641
asthmatic lung ODO3397	29322	10770.42	21540.84	asthmatic lung	25.86121449
asthmatic lung ODO4928	29325	4890.89	9781.78	asthmatic lung	11.74367902
endo cells KC	control	379.58	379.58	endo cells	
endo VEGF KC		308.3	308.30	endo VEGF	-1.231203373
endo bFGF KC		292.91	292.91	endo bFGF	-1.295892936
heart Clontech	normal	189.25	378.50	heart	
heart (T-1) ischemic	29417	3974.32	7948.64	heart T-1	21.00036988
heart (T-14) non-obstructive DCM	29422	2874.83	5749.66	heart T-14	15.19064729
heart (T-3399) DCM	29426	3931.97	7863.94	heart T-3399	20.77659181
adenoid GW99-269	26162	960.03	1920.06	adenoid	
tonsil GW98-280	22582	2921.82	5843.64	tonsil	
T cells PC00314	28453	4357.56	8715.12	T cells	
PBMNC KC		92.93	92.93	PBMNC	
monocyte KC		109.26	218.52	monocyte	

B cells PC00665	28455	2927.24	5854.48	B cells	
dendritic cells 28441		3972.13	7944.26	dendritic cells	
neutrophils	28440	1995.66	1995.66	neutrophils	
eosinophils	28446	3370.63	6741.26	eosinophils	
BM unstim KC		219.27	219.27	BM unstim	
BM stim KC		305.59	305.59	BM stim	1.393669905
osteo dif KC		1240.85	1240.85	osteo dif	
osteo undif KC		250	250.00	osteo undif	-4.9634
chondrocytes		1932.6	4831.50	chondrocytes	
OA Synovium IP12/01	29462	1711.57	1711.57	OA Synovium	
OA Synovium NP10/01	29461	1029.7	2059.40	OA Synovium	
OA Synovium NP57/00	28464	2112.51	4225.02	OA Synovium	
RA Synovium NP03/01	28466	2679.38	5358.76	RA Synovium	
RA Synovium NP71/00	28467	2419.69	4839.38	RA Synovium	
RA Synovium NP45/00	28475	2917.73	5835.46	RA Synovium	
OA bone (biobank)	29217	254.63	254.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	2069.38	4138.76	OA bone	
OA bone Sample 2	J. Emory	1115.3	2230.60	OA bone	
Cartilage (pool)	Normal	3174.67	6349.34	Cartilage (pool)	
Cartilage (pool)	OA	1272.39	2544.78	Cartilage (pool)	-2.495044758
PBL uninfected	28441	4083.14	8166.28	PBL uninfected	
PBL HIV IIIB	28442	1715.44	3430.88	PBL HIV IIIB	-2.380228979
MRC5 uninfected (100%)	29158	6381.95	12763.90	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	759.86	1519.72	MRC5 HSV strain F	-8.398849788
W12 cells	29179	4256.48	8512.96	W12 cells	
Keratinocytes	29180	7993.74	15987.48	Keratinocytes	

Gene Name sbg533677PALSa

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.19
colon tumor	2.03
colon tumor	-1.40
colon tumor	-1.57
lung tumor	-3.95
lung tumor	1.46
lung tumor	-2.27
lung tumor	-1.13
breast tumor	2.99
breast tumor	5.59
breast tumor	4.39
breast tumor	-1.96
brain stage 5 ALZ	-3.76
brain stage 5 ALZ	1.10
brain stage 5 ALZ	-1.46
brain stage 5 ALZ	-1.44

lung 24	-3.81
lung 28	-2.18
lung 23	-3.32
asthmatic lung	1.72
asthmatic lung	8.01
asthmatic lung	25.86
asthmatic lung	11.74
endo VEGF	-1.23
endo bFGF	-1.30
heart T-1	21.00
heart T-14	15.19
heart T-3399	20.78
BM stim	1.39
osteo undif	-4.96
Cartilage (pool)	-2.50
PBL HIV IIIB	-2.38
MRC5 HSV strain F	-8.40

**Gene Name sbg535067MELAa**

- Highest expression in brain (unchanged in alzheimers), fetal liver, and thymus. Downregulated in COPD diseased lung suggesting involvement in this disease. Expression in spleen, T and B cells, neutrophils, and chondrocytes corroborates expression in OA and RA synovium suggesting involvement with OA and RA disease. Upregulated in 3 of 4 asthmatic lung suggesting involvement in asthma. GI tract expression could suggest claims for IBS, IBD, and Crohns disease.

Sample sbg535067MELAa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	23.74	19.92	21.83	3.06	16.34	356.70
Subcutaneous Adipose Zenbio	15.7	3.58	9.64	0.96	52.36	504.71
Adrenal Gland Clontech	1.19	0.43	0.81	0.61	81.97	66.39
Whole Brain Clontech	1924.36	2038.13	1981.25	7.24	6.91	13682.63
Fetal Brain Clontech	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	2.16	5.79	3.98	2.17	23.04	91.59
Cervix	7.08	7.77	7.43	2.42	20.66	153.41
Colon	67.4	68.19	67.80	2.71	18.45	1250.83
Endometrium	4.18	3.42	3.80	0.73	68.21	259.21
Esophagus	15.08	17.4	16.24	1.37	36.50	592.70
Heart Clontech	5.86	14.32	10.09	1.32	37.88	382.20
Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	32.34	66.93	49.64	2.58	19.38	961.92
Jejunum	94.38	105.02	99.70	6.60	7.58	755.30
Kidney	10.77	30.93	20.85	2.12	23.58	491.75

Liver	11.37	10.24	10.81	1.50	33.33	360.17
Fetal Liver Clontech	494.61	735.39	615.00	10.40	4.81	2956.73
Lung	32.92	33.74	33.33	2.57	19.46	648.44
Mammary Gland Clontech	412.57	499.72	456.15	13.00	3.85	1754.40
Myometrium	63.47	115.64	89.56	2.34	21.37	1913.57
Omentum	10.73	13.03	11.88	3.94	12.69	150.76
Ovary	26.09	20.49	23.29	4.34	11.52	268.32
Pancreas	1.74	0.02	0.88	0.81	61.80	54.39
Head of Pancreas	3.26	1.92	2.59	1.57	31.85	82.48
Parotid Gland	19.23	35.41	27.32	5.48	9.12	249.27
Placenta Clontech	117.8	116.55	117.18	5.26	9.51	1113.83
Prostate	10.11	1.88	6.00	3.00	16.67	99.92
Rectum	8.4	8.81	8.61	1.23	40.65	349.80
Salivary Gland Clontech	26.76	14.96	20.86	7.31	6.84	142.68
Skeletal Muscle Clontech	6.71	0	3.36	1.26	39.68	133.13
Skin	11.65	24.94	18.30	1.21	41.32	755.99
Small Intestine Clontech	6.32	11.13	8.73	0.98	51.07	445.61
Spleen	173.46	142.39	157.93	4.92	10.16	1604.93
Stomach	6.64	14.3	10.47	2.73	18.32	191.76
Testis Clontech	8.48	4.71	6.60	0.57	87.87	579.53
Thymus Clontech	544.9	734.52	639.71	9.89	5.06	3234.13
Thyroid	8.81	2.52	5.67	2.77	18.05	102.26
Trachea Clontech	84.46	104.09	94.28	9.71	5.15	485.45
Urinary Bladder	17.47	27.24	22.36	5.47	9.14	204.34
Uterus	40.05	46.49	43.27	5.34	9.36	405.15

Sample sbg535067MELAA	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	614.52	1229.04	colon normal	
colon tumor GW98-166	21940	809.88	1619.76	colon tumor	1.32
colon normal GW98-178	22080	339.76	679.52	colon normal	
colon tumor GW98-177	22060	104.5	209.00	colon tumor	-3.25
colon normal GW98-561	23514	235.88	471.76	colon normal	
colon tumor GW98-560	23513	93.21	186.42	colon tumor	-2.53
colon normal GW98-894	24691	309.33	618.66	colon normal	
colon tumor GW98-893	24690	218.62	437.24	colon tumor	-1.41
lung normal GW98-3	20742	558.13	1116.26	lung normal	
lung tumor GW98-2	20741	82.81	165.62	lung tumor	-6.74
lung normal GW97-179	20677	2066.15	4132.30	lung normal	
lung tumor GW97-178	20676	859.79	1719.58	lung tumor	-2.40
lung normal GW98-165	21922	574.92	1149.84	lung normal	
lung tumor GW98-164	21921	845.89	1691.78	lung tumor	1.47

lung normal GW98-282	22584	210.81	421.62	lung normal	
lung tumor GW98-281	22583	346.75	693.50	lung tumor	1.64
breast normal GW00-392	28750	1165.85	1165.85	breast normal	
breast tumor GW00-391	28746	728.17	1456.34	breast tumor	1.25
breast normal GW00-413	28798	836.13	836.13	breast normal	
breast tumor GW00-412	28797	591.76	1183.52	breast tumor	1.42
breast normal GW00-235:238	27592-95	415.79	415.79	breast normal	
breast tumor GW00-231:234	27588-91	1193.03	1193.03	breast tumor	2.87
breast normal GW98-621	23656	1070.75	2141.50	breast normal	
breast tumor GW98-620	23655	1904.41	3808.82	breast tumor	1.78
brain normal BB99-542	25507	22658.63	45317.26	brain normal	
brain normal BB99-406	25509	4463.72	8927.44	brain normal	
brain normal BB99-904	25546	6799.49	13598.98	brain normal	
brain stage 5 ALZ BB99-874	25502	449.53	899.06	brain stage 5 ALZ	-25.15
brain stage 5 ALZ BB99-887	25503	6199.11	12398.22	brain stage 5 ALZ	-1.82
brain stage 5 ALZ BB99-862	25504	4621.76	9243.52	brain stage 5 ALZ	-2.45
brain stage 5 ALZ BB99-927	25542	4859.74	9719.48	brain stage 5 ALZ	-2.33
CT lung KC	normal	527.05	1054.10	CT lung	
lung 26 KC	normal	628.91	628.91	lung 26	
lung 27 KC	normal	66.78	66.78	lung 27	
lung 24 KC	COPD	45.13	45.13	lung 24	-9.96
lung 28 KC	COPD	64.1	64.10	lung 28	-7.01
lung 23 KC	COPD	97.61	97.61	lung 23	-4.61
lung 25 KC	normal	48.69	48.69	lung 25	
asthmatic lung ODO3112	29321	521.43	521.43	asthmatic lung	1.16
asthmatic lung ODO3433	29323	1614.29	3228.58	asthmatic lung	7.18
asthmatic lung ODO3397	29322	2352.95	4705.90	asthmatic lung	10.47
asthmatic lung ODO4928	29325	1560.6	3121.20	asthmatic lung	6.94
endo cells KC	control	187.93	187.93	endo cells	
endo VEGF KC		30.65	30.65	endo VEGF	-6.13
endo bFGF KC		93.32	93.32	endo bFGF	-2.01
heart Clontech	normal	585.46	1170.92	heart	
heart ( T-1 ) ischemic	29417	1546.85	3093.70	heart T-1	2.64
heart (T-14) non-obstructive DCM	29422	1304.67	2609.34	heart T-14	2.23
heart (T-3399) DCM	29426	2208.72	4417.44	heart T-3399	3.77
adenoid GW99-269	26162	896.42	1792.84	adenoid	
tonsil GW98-280	22582	2459.55	4919.10	tonsil	
T cells PC00314	28453	2147.55	4295.10	T cells	
PBMNC KC		143.16	143.16	PBMNC	
monocyte KC		135.21	270.42	monocyte	

B cells PC00665	28455	1305.96	2611.92	B cells	
dendritic cells 28441		118.25	236.50	dendritic cells	
neutrophils	28440	960.88	960.88	neutrophils	
eosinophils	28446	14.31	28.62	eosinophils	
BM unstim KC		132.56	132.56	BM unstim	
BM stim KC		31.27	31.27	BM stim	-4.24
osteo dif KC		127.45	127.45	osteo dif	2.02
osteo undif KC		63.07	63.07	osteo undif	
chondrocytes		771.65	1929.13	chondrocytes	
OA Synovium IP12/01	29462	2214.8	2214.80	OA Synovium	
OA Synovium NP10/01	29461	576.67	1153.34	OA Synovium	
OA Synovium NP57/00	28464	682.06	1364.12	OA Synovium	
RA Synovium NP03/01	28466	499.99	999.98	RA Synovium	
RA Synovium NP71/00	28467	631.41	1262.82	RA Synovium	
RA Synovium NP45/00	28475	551.2	1102.40	RA Synovium	
OA bone (biobank)	29217	224.68	224.68	OA bone (biobank)	
OA bone Sample 1	J. Emory	751.77	1503.54	OA bone	
OA bone Sample 2	J. Emory	633.33	1266.66	OA bone	
Cartilage (pool)	Normal	1863.02	3726.04	Cartilage (pool)	
Cartilage (pool)	OA	1658.1	3316.20	Cartilage (pool)	-1.12
PBL uninfected	28441	4666.52	9333.04	PBL uninfected	
PBL HIV IIIB	28442	2342.79	4685.58	PBL HIV IIIB	-1.99
MRC5 uninfected (100%)	29158	951.75	1903.50	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	0	0.00	MRC5 HSV strain F	-1903.50
W12 cells	29179	2071.68	4143.36	W12 cells	
Keratinocytes	29180	3752.88	7505.76	Keratinocytes	

Gene Name sbg535067MELAa

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.32
colon tumor	-3.25
colon tumor	-2.53
colon tumor	-1.41
lung tumor	-6.74
lung tumor	-2.40
lung tumor	1.47
lung tumor	1.64
breast tumor	1.25
breast tumor	1.42

breast tumor	2.87
breast tumor	1.78
brain stage 5 ALZ	-25.15
brain stage 5 ALZ	-1.82
brain stage 5 ALZ	-2.45
brain stage 5 ALZ	-2.33
lung 24	-9.96
lung 28	-7.01
lung 23	-4.61
asthmatic lung	1.16
asthmatic lung	7.18
asthmatic lung	10.47
asthmatic lung	6.94
endo VEGF	-6.13
endo bFGF	-2.01
heart T-1	2.64
heart T-14	2.23
heart T-3399	3.77
BM stim	-4.24
osteo dif	2.02
Cartilage (pool)	-1.12
PBL HIV IIIB	-1.99
MRC5 HSV strain F	-1903.50

**Gene Name sbg590979THP**

- 5 High in fetal liver and some expression in adult liver. Expressed in adult and fetal brain. Hypothalamus is a significant fraction of the brain expression suggesting metabolic disease claims related to diabetes, impaired glucose tolerance, metabolic syndrome, and obesity. Significant overexpression in one breast cancer is sufficient for claim in this area (caveat: lack of expression in normal may lead to exaggerated fold-overexpression). Decreased expression in dilated cardiomyopathy suggests involvement in this disease. Expression in OA and RA synovium and
- 10 corroborating expression in immune cells (adenoid, tonsil, T, B, and eosinophils) suggests involvement in both RA and OA disease. Significant decrease in DCM heart suggests involvement in dilated cardiomyopathy.

Sample sbg590979THP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00



Whole Brain Clontech	103.17	92.02	97.60	7.24	6.91	674.00
Fetal Brain Clontech	0	5.32	2.66	0.48	103.95	276.51
Cerebellum Clontech	0	0	0.00	2.17	23.04	0.00
Cervix	0	0	0.00	2.42	20.66	0.00
Colon	5.58	4.45	5.02	2.71	18.45	92.53
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	4.11	2.06	1.32	37.88	77.84
Hypothalamus	4.16	0	2.08	0.32	155.28	322.98
Ileum	0	7.16	3.58	2.58	19.38	69.38
Jejunum	3.15	8.34	5.75	6.60	7.58	43.52
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	17.8	29.95	23.88	1.50	33.33	795.83
Fetal Liver Clontech	2349.79	2396.71	2373.25	10.40	4.81	11409.86
Lung	9.75	0	4.88	2.57	19.46	94.84
Mammary Gland Clontech	0	0	0.00	13.00	3.85	0.00
Myometrium	0	0	0.00	2.34	21.37	0.00
Omentum	0	0	0.00	3.94	12.69	0.00
Ovary	12.64	21.85	17.25	4.34	11.52	198.68
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	17.64	0	8.82	5.48	9.12	80.47
Placenta Clontech	2.66	0	1.33	5.26	9.51	12.64
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	3.58	0	1.79	7.31	6.84	12.24
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	14.01	13.8	13.91	4.92	10.16	141.31
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	0	13.24	6.62	9.89	5.06	33.47
Thyroid	10.53	0	5.27	2.77	18.05	95.04
Trachea Clontech	0	9.3	4.65	9.71	5.15	23.94
Urinary Bladder	0	0	0.00	5.47	9.14	0.00
Uterus	13.93	6.43	10.18	5.34	9.36	95.32

Sample sbg590979THP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	148.83	297.66	colon normal	
colon tumor GW98-166	21940	246.62	493.24	colon tumor	1.66
colon normal GW98-178	22080	97.46	194.92	colon normal	
colon tumor GW98-177	22060	68.77	137.54	colon tumor	-1.42

colon normal GW98-561	23514	210.78	421.56	colon normal	
colon tumor GW98-560	23513	76.83	153.66	colon tumor	-2.74
colon normal GW98-894	24691	130.52	261.04	colon normal	
colon tumor GW98-893	24690	89.49	178.98	colon tumor	-1.46
lung normal GW98-3	20742	108.75	217.50	lung normal	
lung tumor GW98-2	20741	9.94	19.88	lung tumor	-10.94
lung normal GW97-179	20677	39.37	78.74	lung normal	
lung tumor GW97-178	20676	34.84	69.68	lung tumor	-1.13
lung normal GW98-165	21922	54.25	108.50	lung normal	
lung tumor GW98-164	21921	153.78	307.56	lung tumor	2.83
lung normal GW98-282	22584	61.06	122.12	lung normal	
lung tumor GW98-281	22583	42.22	84.44	lung tumor	-1.45
breast normal GW00-392	28750	23.64	23.64	breast normal	
breast tumor GW00-391	28746	24.54	49.08	breast tumor	2.08
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	19.55	39.10	breast tumor	39.10
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	18.18	36.36	breast normal	
breast tumor GW98-620	23655	78.46	156.92	breast tumor	4.32
brain normal BB99-542	25507	31.51	63.02	brain normal	
brain normal BB99-406	25509	39.55	79.10	brain normal	
brain normal BB99-904	25546	3.64	7.28	brain normal	
brain stage 5 ALZ BB99-874	25502	25.84	51.68	brain stage 5 ALZ	1.04
brain stage 5 ALZ BB99-887	25503	98.79	197.58	brain stage 5 ALZ	3.97
brain stage 5 ALZ BB99-862	25504	43.27	86.54	brain stage 5 ALZ	1.74
brain stage 5 ALZ BB99-927	25542	56.03	112.06	brain stage 5 ALZ	2.25
CT lung KC	normal	7.59	15.18	CT lung	
lung 26 KC	normal	0	0.00	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-3.80
lung 28 KC	COPD	0	0.00	lung 28	-3.80
lung 23 KC	COPD	3.41	3.41	lung 23	-1.11
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0	0.00	asthmatic lung	-3.80
asthmatic lung ODO3433	29323	7	14.00	asthmatic lung	3.69
asthmatic lung ODO3397	29322	14.33	28.66	asthmatic lung	7.55
asthmatic lung ODO4928	29325	7.81	15.62	asthmatic lung	4.12
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		2.17	2.17	endo VEGF	2.17
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	58.56	117.12	heart	
heart ( T-1 ) ischemic	29417	40.59	81.18	heart T-1	-1.44

heart (T-14) non-obstructive DCM	29422	180.2	360.40	heart T-14	3.08
heart (T-3399) DCM	29426	0	0.00	heart T-3399	-117.12
adenoid GW99-269	26162	25.38	50.76	adenoid	
tonsil GW98-280	22582	31.19	62.38	tonsil	
T cells PC00314	28453	25.24	50.48	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		1.43	2.86	monocyte	
B cells PC00665	28455	20.91	41.82	B cells	
dendritic cells 28441		0	0.00	dendritic cells	
neutrophils	28440	20.88	20.88	neutrophils	
eosinophils	28446	31.73	63.46	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		9.9	9.90	BM stim	9.90
osteo dif KC		3.62	3.62	osteo dif	3.62
osteo undif KC		0	0.00	osteo undif	
chondrocytes		26.14	65.35	chondrocytes	
OA Synovium IP12/01	29462	25.64	25.64	OA Synovium	
OA Synovium NP10/01	29461	52	104.00	OA Synovium	
OA Synovium NP57/00	28464	90.32	180.64	OA Synovium	
RA Synovium NP03/01	28466	64.83	129.66	RA Synovium	
RA Synovium NP71/00	28467	321.14	642.28	RA Synovium	
RA Synovium NP45/00	28475	91.05	182.10	RA Synovium	
OA bone (biobank)	29217	10.58	10.58	OA bone (biobank)	
OA bone Sample 1	J. Emory	41.46	82.92	OA bone	
OA bone Sample 2	J. Emory	82	164.00	OA bone	
Cartilage (pool)	Normal	12.72	25.44	Cartilage (pool)	
Cartilage (pool)	OA	45.45	90.90	Cartilage (pool)	3.57
PBL uninfected	28441	18.32	36.64	PBL uninfected	
PBL HIV IIIB	28442	46.38	92.76	PBL HIV IIIB	2.53
MRC5 uninfected (100%)	29158	10.17	20.34	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	424.91	849.82	MRC5 HSV strain F	41.78
W12 cells	29179	12.35	24.70	W12 cells	
Keratinocytes	29180	11.74	23.48	Keratinocytes	

Gene Name sbg590979THP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.66
colon tumor	-1.42
colon tumor	-2.74
colon tumor	-1.46
lung tumor	-10.94
lung tumor	-1.13

lung tumor	2.83
lung tumor	-1.45
breast tumor	2.08
breast tumor	39.10
breast tumor	0.00
breast tumor	4.32
brain stage 5 ALZ	1.04
brain stage 5 ALZ	3.97
brain stage 5 ALZ	1.74
brain stage 5 ALZ	2.25
lung 24	-3.80
lung 28	-3.80
lung 23	-1.11
asthmatic lung	-3.80
asthmatic lung	3.69
asthmatic lung	7.55
asthmatic lung	4.12
endo VEGF	2.17
endo bFGF	0.00
heart T-1	-1.44
heart T-14	3.08
heart T-3399	-117.12
BM stim	9.90
osteo dif	3.62
Cartilage (pool)	3.57
PBL HIV IIIB	2.53
MRC5 HSV strain F	41.78

**Gene Name sbg658629CRF**

- 5 Highly expressed in brain. Expression in parotid gland suggest it is secreted.  
 Expression in chondrocyte cells consistent with expression in cartilage.  
 Downregulated in HSV infected MRC5 cells suggesting possible host factor for HSV infection.

Sample sbg658629CRF	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0.41	0.12	0.27	3.06	16.34	4.33
Subcutaneous Adipose Zenbio	0.26	0	0.13	0.96	52.36	6.81
Adrenal Gland Clontech	0	0.04	0.02	0.61	81.97	1.64
Whole Brain Clontech	8417.5	9519.49	8968.50	7.24	6.91	61937.12
Fetal Brain Clontech	8.6	10.03	9.32	0.48	103.95	968.30
Cerebellum Clontech	12.11	12.1	12.11	2.17	23.04	278.92
Cervix	2.83	5.55	4.19	2.42	20.66	86.57
Colon	4.92	1.31	3.12	2.71	18.45	57.47
Endometrium	5.14	9.68	7.41	0.73	68.21	505.46

Esophagus	0.11	0.14	0.13	1.37	36.50	4.56
Heart Clontech	0	1.03	0.52	1.32	37.88	19.51
Hypothalamus	0	0.27	0.14	0.32	155.28	20.96
Ileum	3.59	1.4	2.50	2.58	19.38	48.35
Jejunum	20.07	31.06	25.57	6.60	7.58	193.67
Kidney	2.83	7.94	5.39	2.12	23.58	127.00
Liver	4.23	7.95	6.09	1.50	33.33	203.00
Fetal Liver Clontech	16.66	25.88	21.27	10.40	4.81	102.26
Lung	1.42	1.64	1.53	2.57	19.46	29.77
Mammary Gland Clontech	3.1	9.56	6.33	13.00	3.85	24.35
Myometrium	2.87	3.05	2.96	2.34	21.37	63.25
Omentum	2.76	3.5	3.13	3.94	12.69	39.72
Ovary	9.43	10.74	10.09	4.34	11.52	116.19
Pancreas	0.88	0.04	0.46	0.81	61.80	28.43
Head of Pancreas	0.04	0.12	0.08	1.57	31.85	2.55
Parotid Gland	368.36	439.47	403.92	5.48	9.12	3685.36
Placenta Clontech	2.99	0.93	1.96	5.26	9.51	18.63
Prostate	0.15	0.06	0.11	3.00	16.67	1.75
Rectum	1.08	1.78	1.43	1.23	40.65	58.13
Salivary Gland Clontech	0.76	1.35	1.06	7.31	6.84	7.22
Skeletal Muscle Clontech	0.2	0.07	0.14	1.26	39.68	5.36
Skin	0.03	0.05	0.04	1.21	41.32	1.65
Small Intestine Clontech	7.1	0.03	3.57	0.98	51.07	182.07
Spleen	2.3	0.03	1.23	4.92	10.16	12.45
Stomach	3.63	4.6	4.12	2.73	18.32	75.37
Testis Clontech	8.57	4.18	6.38	0.57	87.87	560.19
Thymus Clontech	5.54	16.02	10.78	9.89	5.06	54.50
Thyroid	12.12	4.34	8.23	2.77	18.05	148.56
Trachea Clontech	3.97	17.75	10.86	9.71	5.15	55.92
Urinary Bladder	5.08	8.59	6.84	5.47	9.14	62.48
Uterus	24.16	29.46	26.81	5.34	9.36	251.03

Sample sbg658629CRF	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	758.1	1516.20	colon normal	
colon tumor GW98-166	21940	77.72	155.44	colon tumor	-9.75
colon normal GW98-178	22080	364.17	728.34	colon normal	
colon tumor GW98-177	22060	85.55	171.10	colon tumor	-4.26
colon normal GW98-561	23514	227.04	454.08	colon normal	
colon tumor GW98-560	23513	294.95	589.90	colon tumor	1.30
colon normal GW98-894	24691	521.04	1042.08	colon normal	
colon tumor GW98-893	24690	194.26	388.52	colon tumor	-2.68
lung normal GW98-3	20742	86.31	172.62	lung normal	
lung tumor GW98-2	20741	158.3	316.60	lung tumor	1.83

lung normal GW97-179	20677	3312.4	6624.80	lung normal	
lung tumor GW97-178	20676	27.8	55.60	lung tumor	-119.15
lung normal GW98-165	21922	17.58	35.16	lung normal	
lung tumor GW98-164	21921	56.57	113.14	lung tumor	3.22
lung normal GW98-282	22584	48.66	97.32	lung normal	
lung tumor GW98-281	22583	30.43	60.86	lung tumor	-1.60
breast normal GW00-392	28750	226.72	226.72	breast normal	
breast tumor GW00-391	28746	181.98	363.96	breast tumor	1.61
breast normal GW00-413	28798	84.66	84.66	breast normal	
breast tumor GW00-412	28797	43.27	86.54	breast tumor	1.02
breast normal GW00-235:238	27592-95	266.41	266.41	breast normal	
breast tumor GW00-231:234	27588-91	71.99	71.99	breast tumor	-3.70
breast normal GW98-621	23656	167.13	334.26	breast normal	
breast tumor GW98-620	23655	63.98	127.96	breast tumor	-2.61
brain normal BB99-542	25507	2057.45	4114.90	brain normal	
brain normal BB99-406	25509	1914.41	3828.82	brain normal	
brain normal BB99-904	25546	1209.14	2418.28	brain normal	
brain stage 5 ALZ BB99-874	25502	1126.82	2253.64	brain stage 5 ALZ	-1.53
brain stage 5 ALZ BB99-887	25503	4130.76	8261.52	brain stage 5 ALZ	2.39
brain stage 5 ALZ BB99-862	25504	3025.26	6050.52	brain stage 5 ALZ	1.75
brain stage 5 ALZ BB99-927	25542	1582.92	3165.84	brain stage 5 ALZ	-1.09
CT lung KC	normal	26.49	52.98	CT lung	
lung 26 KC	normal	10.85	10.85	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-16.04
lung 28 KC	COPD	0.74	0.74	lung 28	-21.68
lung 23 KC	COPD	0	0.00	lung 23	-16.04
lung 25 KC	normal	0.33	0.33	lung 25	
asthmatic lung ODO3112	29321	5.95	5.95	asthmatic lung	-2.70
asthmatic lung ODO3433	29323	16.33	32.66	asthmatic lung	2.04
asthmatic lung ODO3397	29322	25.26	50.52	asthmatic lung	3.15
asthmatic lung ODO4928	29325	20.78	41.56	asthmatic lung	2.59
endo cells KC	control	15.55	15.55	endo cells	
endo VEGF KC		6.35	6.35	endo VEGF	-2.45
endo bFGF KC		19.16	19.16	endo bFGF	1.23
heart Clontech	normal	312.58	625.16	heart	
heart (T-1) ischemic	29417	107.41	214.82	heart T-1	-2.91
heart (T-14) non-obstructive DCM	29422	65.45	130.90	heart T-14	-4.78
heart (T-3399) DCM	29426	80.9	161.80	heart T-3399	-3.86
adenoid GW99-269	26162	11.42	22.84	adenoid	
tonsil GW98-280	22582	58.08	116.16	tonsil	
T cells PC00314	28453	13.31	26.62	T cells	

PBMNC KC		0.18	0.18	PBMNC	
monocyte KC		0.45	0.90	monocyte	
B cells PC00665	28455	2.47	4.94	B cells	
dendritic cells 28441		19.58	39.16	dendritic cells	
neutrophils	28440	4.52	4.52	neutrophils	
eosinophils	28446	7.41	14.82	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		8.97	8.97	BM stim	8.97
osteo dif KC		0.56	0.56	osteo dif	-1.43
osteo undif KC		0.8	0.80	osteo undif	
chondrocytes		547.4	1368.50	chondrocytes	
OA Synovium IP12/01	29462	157.16	157.16	OA Synovium	
OA Synovium NP10/01	29461	46.09	92.18	OA Synovium	
OA Synovium NP57/00	28464	63.76	127.52	OA Synovium	
RA Synovium NP03/01	28466	64.6	129.20	RA Synovium	
RA Synovium NP71/00	28467	200.22	400.44	RA Synovium	
RA Synovium NP45/00	28475	189.2	378.40	RA Synovium	
OA bone (biobank)	29217	34.76	34.76	OA bone (biobank)	
OA bone Sample 1	J. Emory	114.88	229.76	OA bone	
OA bone Sample 2	J. Emory	34.93	69.86	OA bone	
Cartilage (pool)	Normal	750.07	1500.14	Cartilage (pool)	
Cartilage (pool)	OA	107.9	215.80	Cartilage (pool)	-6.95
PBL uninfected	28441	196.14	392.28	PBL uninfected	
PBL HIV IIIB	28442	120.64	241.28	PBL HIV IIIB	-1.63
MRC5 uninfected (100%)	29158	1065.06	2130.12	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	179.4	358.80	MRC5 HSV strain F	-5.94
W12 cells	29179	127.4	254.80	W12 cells	
Keratinocytes	29180	92.44	184.88	Keratinocytes	

Gene Name sbg658629CRF

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-9.75
colon tumor	-4.26
colon tumor	1.30
colon tumor	-2.68
lung tumor	1.83
lung tumor	-119.15
lung tumor	3.22
lung tumor	-1.60
breast tumor	1.61
breast tumor	1.02
breast tumor	-3.70

breast tumor	-2.61
brain stage 5 ALZ	-1.53
brain stage 5 ALZ	2.39
brain stage 5 ALZ	1.75
brain stage 5 ALZ	-1.09
lung 24	-16.04
lung 28	-21.68
lung 23	-16.04
asthmatic lung	-2.70
asthmatic lung	2.04
asthmatic lung	3.15
asthmatic lung	2.59
endo VEGF	-2.45
endo bFGF	1.23
heart T-1	-2.91
heart T-14	-4.78
heart T-3399	-3.86
BM stim	8.97
osteo dif	-1.43
Cartilage (pool)	-6.95
PBL HIV IIIB	-1.63
MRC5 HSV strain F	-5.94

**Gene Name sbg507131mannosidase**

Expressed in brain, especially cortex, but not changed in alzheimers. Expressed in subcutaneous adipose and adipocytes. Expression in fetal liver, thymus, and immune cell populations (adenoid, tonsil, eosinophils, neutrophils, T cells, B cells, and dendritic cells) suggest some involvement in immune cell functions. Expression in asthmatic lung although not significantly upregulated compared to clontech pool. Expressed in OA and RA synovium, OA bone, cartilage, and chondrocytes suggests involvement in OA and RA. Significantly downregulated in HSV lung cell line suggests possible host factor for HSV infection. Expression in subcutaneous adipose suggests claim for dyslipidemia and obesity.

Sample sbg507131mannosidase	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	157.3	180.21	168.76	3.06	16.34	2757.43
Subcutaneous Adipose Zenbio	27.08	7.08	17.08	0.96	52.36	894.24
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	8341.44	12017.65	10179.55	7.24	6.91	70300.73
Fetal Brain Clontech	11.48	15.85	13.67	0.48	103.95	1420.48
Cerebellum Clontech	10.53	9.03	9.78	2.17	23.04	225.35
Cervix	23.6	11.58	17.59	2.42	20.66	363.43
Colon	38.31	72.55	55.43	2.71	18.45	1022.69
Endometrium	15.99	21.62	18.81	0.73	68.21	1282.74
Esophagus	6.27	7.28	6.78	1.37	36.50	247.26
Heart Clontech	0	8.15	4.08	1.32	37.88	154.36
Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	6.58	11.07	8.83	2.58	19.38	171.03



Jejunum	38.74	51.43	45.09	6.60	7.58	341.55
Kidney	20.7	26.62	23.66	2.12	23.58	558.02
Liver	16.74	15.49	16.12	1.50	33.33	537.17
Fetal Liver Clontech	876.2	881.14	878.67	10.40	4.81	4224.38
Lung	0	9.21	4.61	2.57	19.46	89.59
Mammary Gland Clontech	168.63	218.21	193.42	13.00	3.85	743.92
Myometrium	30.45	12.65	21.55	2.34	21.37	460.47
Omentum	10.92	0	5.46	3.94	12.69	69.29
Ovary	78.21	48.52	63.37	4.34	11.52	730.01
Pancreas	0.83	0.38	0.61	0.81	61.80	37.39
Head of Pancreas	0.45	0	0.23	1.57	31.85	7.17
Parotid Gland	28.48	86.17	57.33	5.48	9.12	523.04
Placenta Clontech	49.24	92.67	70.96	5.26	9.51	674.48
Prostate	31.41	22.64	27.03	3.00	16.67	450.42
Rectum	27.38	23.01	25.20	1.23	40.65	1024.19
Salivary Gland Clontech	64.88	84.19	74.54	7.31	6.84	509.82
Skeletal Muscle Clontech	0.88	0.38	0.63	1.26	39.68	25.00
Skin	0	0.44	0.22	1.21	41.32	9.09
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	28.32	10.16	19.24	4.92	10.16	195.53
Stomach	0.49	11.86	6.18	2.73	18.32	113.10
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	992.36	1311.32	1151.84	9.89	5.06	5823.26
Thyroid	5.25	29.51	17.38	2.77	18.05	313.72
Trachea Clontech	96.02	82.56	89.29	9.71	5.15	459.78
Urinary Bladder	22.05	34.45	28.25	5.47	9.14	258.23
Uterus	74.02	95.43	84.73	5.34	9.36	793.31

Sample sbg507131mannosidase	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	9614.3	19228.60	colon normal	
colon tumor GW98-166	21940	16103.87	32207.74	colon tumor	1.67
colon normal GW98-178	22080	2303.04	4606.08	colon normal	
colon tumor GW98-177	22060	5088.22	10176.44	colon tumor	2.21
colon normal GW98-561	23514	9405.12	18810.24	colon normal	
colon tumor GW98-560	23513	7410.97	14821.94	colon tumor	-1.27
colon normal GW98-894	24691	17796.08	35592.16	colon normal	
colon tumor GW98-893	24690	11212.12	22424.24	colon tumor	-1.59
lung normal GW98-3	20742	27285.1	54570.20	lung normal	
lung tumor GW98-2	20741	4815.29	9630.58	lung tumor	-5.67
lung normal GW97-179	20677	10640.73	21281.46	lung normal	
lung tumor GW97-178	20676	13513.23	27026.46	lung tumor	1.27
lung normal GW98-165	21922	9994.82	19989.64	lung normal	
lung tumor GW98-164	21921	10116.17	20232.34	lung tumor	1.01

lung normal GW98-282	22584	3301.07	6602.14	lung normal	
lung tumor GW98-281	22583	4877.02	9754.04	lung tumor	1.48
breast normal GW00-392	28750	4720.46	4720.46	breast normal	
breast tumor GW00-391	28746	4546.76	9093.52	breast tumor	1.93
breast normal GW00-413	28798	2621.82	2621.82	breast normal	
breast tumor GW00-412	28797	6120.14	12240.28	breast tumor	4.67
breast normal GW00-235:238	27592-95	1687.45	1687.45	breast normal	
breast tumor GW00-231:234	27588-91	5583.72	5583.72	breast tumor	3.31
breast normal GW98-621	23656	5377.79	10755.58	breast normal	
breast tumor GW98-620	23655	4502.23	9004.46	breast tumor	-1.19
brain normal BB99-542	25507	6715.69	13431.38	brain normal	
brain normal BB99-406	25509	5048.43	10096.86	brain normal	
brain normal BB99-904	25546	5145.09	10290.18	brain normal	
brain stage 5 ALZ BB99-874	25502	2895.87	5791.74	brain stage 5 ALZ	-1.95
brain stage 5 ALZ BB99-887	25503	7573.41	15146.82	brain stage 5 ALZ	1.34
brain stage 5 ALZ BB99-862	25504	5549.18	11098.36	brain stage 5 ALZ	-1.02
brain stage 5 ALZ BB99-927	25542	7409.43	14818.86	brain stage 5 ALZ	1.31
CT lung KC	normal	5550.23	11100.46	CT lung	
lung 26 KC	normal	148.79	148.79	lung 26	
lung 27 KC	normal	69.13	69.13	lung 27	
lung 24 KC	COPD	85.09	85.09	lung 24	-33.61
lung 28 KC	COPD	122.28	122.28	lung 28	-23.39
lung 23 KC	COPD	83.08	83.08	lung 23	-34.42
lung 25 KC	normal	121.14	121.14	lung 25	
asthmatic lung ODO3112	29321	2772.08	2772.08	asthmatic lung	-1.03
asthmatic lung ODO3433	29323	4996.38	9992.76	asthmatic lung	3.49
asthmatic lung ODO3397	29322	9994.38	19988.76	asthmatic lung	6.99
asthmatic lung ODO4928	29325	6018.96	12037.92	asthmatic lung	4.21
endo cells KC	control	428.24	428.24	endo cells	
endo VEGF KC		535	535.00	endo VEGF	1.25
endo bFGF KC		323.01	323.01	endo bFGF	-1.33
heart Clontech	normal	2610.15	5220.30	heart	
heart ( T-1 ) ischemic	29417	4004.99	8009.98	heart T-1	1.53
heart (T-14) non-obstructive DCM	29422	5596.98	11193.96	heart T-14	2.14
heart (T-3399) DCM	29426	9381.53	18763.06	heart T-3399	3.59
adenoid GW99-269	26162	4435.48	8870.96	adenoid	
tonsil GW98-280	22582	7399.53	14799.06	tonsil	
T cells PC00314	28453	6576.4	13152.80	T cells	
PBMNC KC		139.42	139.42	PBMNC	
monocyte KC		126.02	252.04	monocyte	
B cells PC00665	28455	9735.42	19470.84	B cells	
dendritic cells 28441		15293.67	30587.34	dendritic cells	

neutrophils	28440	13487.07	13487.07	neutrophils	
eosinophils	28446	13111.46	26222.92	eosinophils	
BM unstim KC		332.7	332.70	BM unstim	
BM stim KC		379.27	379.27	BM stim	1.14
osteo dif KC		427.84	427.84	osteo dif	1.60
osteo undif KC		267.96	267.96	osteo undif	
chondrocytes		7063.55	17658.88	chondrocytes	
OA Synovium IP12/01	29462	9069.17	9069.17	OA Synovium	
OA Synovium NP10/01	29461	4247.36	8494.72	OA Synovium	
OA Synovium NP57/00	28464	4826.09	9652.18	OA Synovium	
RA Synovium NP03/01	28466	6003.36	12006.72	RA Synovium	
RA Synovium NP71/00	28467	6850.62	13701.24	RA Synovium	
RA Synovium NP45/00	28475	8737.59	17475.18	RA Synovium	
OA bone (biobank)	29217	3479.78	3479.78	OA bone (biobank)	
OA bone Sample 1	J. Emory	2992.04	5984.08	OA bone	
OA bone Sample 2	J. Emory	5164.14	10328.28	OA bone	
Cartilage (pool)	Normal	7859.28	15718.56	Cartilage (pool)	
Cartilage (pool)	OA	4341.01	8682.02	Cartilage (pool)	-1.81
PBL uninfected	28441	16983.2	33966.40	PBL uninfected	
PBL HIV IIIB	28442	9427.01	18854.02	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	17734.85	35469.70	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	670.02	1340.04	MRC5 HSV strain F	-26.47
W12 cells	29179	3619.54	7239.08	W12 cells	
Keratinocytes	29180	4955.73	9911.46	Keratinocytes	

Gene Name sbg507131mannosidase

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.67
colon tumor	2.21
colon tumor	-1.27
colon tumor	-1.59
lung tumor	-5.67
lung tumor	1.27
lung tumor	1.01
lung tumor	1.48
breast tumor	1.93
breast tumor	4.67
breast tumor	3.31
breast tumor	-1.19
brain stage 5 ALZ	-1.95
brain stage 5 ALZ	1.34
brain stage 5 ALZ	-1.02
brain stage 5 ALZ	1.31

lung 24	-33.61
lung 28	-23.39
lung 23	-34.42
asthmatic lung	-1.03
asthmatic lung	3.49
asthmatic lung	6.99
asthmatic lung	4.21
endo VEGF	1.25
endo bFGF	-1.33
heart T-1	1.53
heart T-14	2.14
heart T-3399	3.59
BM stim	1.14
osteo dif	1.60
Cartilage (pool)	-1.81
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-26.47

**Gene Name sbg655871calgizzarin-like**

High expression in brain. Expression in intestines along with immune expression suggest claims for IBS, IBD, and crohn's disease. Fetal liver, thymus, adenoid, tonsil, T and

- 5 B cells and monocytes corroborates immune cell expression. Expression in RA and OA synovium and OA bone suggests involvement in these diseases. Significant overexpression in one breast tumor is sufficient to claim breast cancer (caveat: undetectable expression in normal may lead to exaggerated fold-overexpression). Consistently higher expression in normal adjacent and tumor tissue compared to tissues on normal masterplate is also
- 10 consistent with expression in activated immune cells.

Sample sbg655871calgizzarin-like	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	537.46	799.45	668.46	7.24	6.91	4616.40
Fetal Brain Clontech	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	29.9	13.65	21.78	2.17	23.04	501.73
Cervix	0	0	0.00	2.42	20.66	0.00
Colon	15.41	16.6	16.01	2.71	18.45	295.30
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	0	0.00	1.32	37.88	0.00

Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	0	15.15	7.58	2.58	19.38	146.80
Jejunum	40.86	16.79	28.83	6.60	7.58	218.37
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	0	12.5	6.25	1.50	33.33	208.33
Fetal Liver Clontech	293.5	393.13	343.32	10.40	4.81	1650.55
Lung	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	91.08	118.14	104.61	13.00	3.85	402.35
Myometrium	0	26.43	13.22	2.34	21.37	282.37
Omentum	0	0	0.00	3.94	12.69	0.00
Ovary	22.65	12.76	17.71	4.34	11.52	203.97
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	23.32	24.07	23.70	5.48	9.12	216.20
Placenta Clontech	28.2	34.71	31.46	5.26	9.51	299.00
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	52.48	55.96	54.22	7.31	6.84	370.86
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	13.83	0	6.92	4.92	10.16	70.27
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	409.4	502.34	455.87	9.89	5.06	2304.70
Thyroid	22.55	17.24	19.90	2.77	18.05	359.12
Trachea Clontech	73.02	52.6	62.81	9.71	5.15	323.43
Urinary Bladder	0	0	0.00	5.47	9.14	0.00
Uterus	0	24.54	12.27	5.34	9.36	114.89

Sample sbg655871calgizzarin- like	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	263.68	527.36	colon normal	
colon tumor GW98-166	21940	566.89	1133.78	colon tumor	2.15
colon normal GW98-178	22080	48.87	97.74	colon normal	
colon tumor GW98-177	22060	188.64	377.28	colon tumor	3.86
colon normal GW98-561	23514	113.25	226.50	colon normal	
colon tumor GW98-560	23513	196.14	392.28	colon tumor	1.73
colon normal GW98-894	24691	318.81	637.62	colon normal	
colon tumor GW98-893	24690	460.8	921.60	colon tumor	1.45
lung normal GW98-3	20742	508.76	1017.52	lung normal	

lung tumor GW98-2	20741	124.1	248.20	lung tumor	-4.10
lung normal GW97-179	20677	601.78	1203.56	lung normal	
lung tumor GW97-178	20676	316.85	633.70	lung tumor	-1.90
lung normal GW98-165	21922	913.61	1827.22	lung normal	
lung tumor GW98-164	21921	747.36	1494.72	lung tumor	-1.22
lung normal GW98-282	22584	216.1	432.20	lung normal	
lung tumor GW98-281	22583	177.97	355.94	lung tumor	-1.21
breast normal GW00-392	28750	186.88	186.88	breast normal	
breast tumor GW00-391	28746	278.12	556.24	breast tumor	2.98
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	804.19	1608.38	breast tumor	1608.38
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	716.41	1432.82	breast normal	
breast tumor GW98-620	23655	436.65	873.30	breast tumor	-1.64
brain normal BB99-542	25507	404.96	809.92	brain normal	
brain normal BB99-406	25509	496.2	992.40	brain normal	
brain normal BB99-904	25546	90.22	180.44	brain normal	
brain stage 5 ALZ BB99-874	25502	90.86	181.72	brain stage 5 ALZ	-3.64
brain stage 5 ALZ BB99-887	25503	379.2	758.40	brain stage 5 ALZ	1.15
brain stage 5 ALZ BB99-862	25504	278.99	557.98	brain stage 5 ALZ	-1.18
brain stage 5 ALZ BB99-927	25542	316.21	632.42	brain stage 5 ALZ	-1.05
CT lung KC	normal	260.58	521.16	CT lung	
lung 26 KC	normal	0	0.00	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-130.29
lung 28 KC	COPD	0	0.00	lung 28	-130.29
lung 23 KC	COPD	0	0.00	lung 23	-130.29
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0	0.00	asthmatic lung	-130.29
asthmatic lung ODO3433	29323	25.9	51.80	asthmatic lung	-2.52
asthmatic lung ODO3397	29322	274.29	548.58	asthmatic lung	4.21
asthmatic lung ODO4928	29325	76.05	152.10	asthmatic lung	1.17
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		15.57	15.57	endo VEGF	15.57
endo bFGF KC		24.36	24.36	endo bFGF	24.36
heart Clontech	normal	0	0.00	heart	
heart ( T-1 ) ischemic	29417	286.72	573.44	heart T-1	573.44
heart (T-14) non-obstructive DCM	29422	160.22	320.44	heart T-14	320.44
heart (T-3399) DCM	29426	212.95	425.90	heart T-3399	425.90
adenoid GW99-269	26162	404.24	808.48	adenoid	
tonsil GW98-280	22582	1077.53	2155.06	tonsil	

T cells PC00314	28453	562.08	1124.16	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		0	0.00	monocyte	
B cells PC00665	28455	925.74	1851.48	B cells	
dendritic cells 28441		56.59	113.18	dendritic cells	
neutrophils	28440	83.29	83.29	neutrophils	
eosinophils	28446	399.07	798.14	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		24.03	24.03	BM stim	24.03
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		59.55	148.88	chondrocytes	
OA Synovium IP12/01	29462	17.31	17.31	OA Synovium	
OA Synovium NP10/01	29461	222.82	445.64	OA Synovium	
OA Synovium NP57/00	28464	267.63	535.26	OA Synovium	
RA Synovium NP03/01	28466	227.09	454.18	RA Synovium	
RA Synovium NP71/00	28467	638.53	1277.06	RA Synovium	
RA Synovium NP45/00	28475	1088.59	2177.18	RA Synovium	
OA bone (biobank)	29217	66.45	66.45	OA bone (biobank)	
OA bone Sample 1	J. Emory	205.74	411.48	OA bone	
OA bone Sample 2	J. Emory	679.55	1359.10	OA bone	
Cartilage (pool)	Normal	736.08	1472.16	Cartilage (pool)	
Cartilage (pool)	OA	286.47	572.94	Cartilage (pool)	-2.57
PBL uninfected	28441	1155.62	2311.24	PBL uninfected	
PBL HIV IIIB	28442	763.53	1527.06	PBL HIV IIIB	-1.51
MRC5 uninfected (100%)	29158	97.19	194.38	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.38	60.76	MRC5 HSV strain F	-3.20
W12 cells	29179	182.95	365.90	W12 cells	
Keratinocytes	29180	211.73	423.46	Keratinocytes	

Gene Name sbg655871calgizzarin-like

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	2.15
colon tumor	3.86
colon tumor	1.73
colon tumor	1.45
lung tumor	-4.10
lung tumor	-1.90
lung tumor	-1.22
lung tumor	-1.21
breast tumor	2.98
breast tumor	1608.38

breast tumor	0.00
breast tumor	-1.64
brain stage 5 ALZ	-3.64
brain stage 5 ALZ	1.15
brain stage 5 ALZ	-1.18
brain stage 5 ALZ	-1.05
lung 24	-130.29
lung 28	-130.29
lung 23	-130.29
asthmatic lung	-130.29
asthmatic lung	-2.52
asthmatic lung	4.21
asthmatic lung	1.17
endo VEGF	15.57
endo bFGF	24.36
heart T-1	573.44
heart T-14	320.44
heart T-3399	425.90
BM stim	24.03
osteo dif	0.00
Cartilage (pool)	-2.57
PBL HIV IIIB	-1.51
MRC5 HSV strain F	-3.20

**Gene Name sbg506454MPG-1**

Significant upregulation in one breast adenocarcinoma sufficient to make a claim for breast cancer. Widespread expression in immune cell populations, upregulated expression in 3 of 4 asthmatic lungs and high expression in RA and OA synovium, OA bone and cartilage suggest involvement in asthma, OA, and RA disease. Expression in GI tract as well as subcutaneous adipose suggest claims in IBS, IBD, and crohn's diseases. Expression in subcutaneous adipose and omentum (a fat depot) suggests claim for dyslipidemia and obesity.

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Sample sbg506454MPG-1	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	32.46	22.02	27.24	3.06	16.34	445.10
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	9195.49	12359.11	10777.30	7.24	6.91	74428.87
Fetal Brain Clontech	8.14	12.95	10.55	0.48	103.95	1096.15
Cerebellum Clontech	161.39	87.85	124.62	2.17	23.04	2871.43
Cervix	58.73	35.95	47.34	2.42	20.66	978.10
Colon	11.75	41.67	26.71	2.71	18.45	492.80



Endometrium	0	15.54	7.77	0.73	68.21	530.01
Esophagus	0	12.09	6.05	1.37	36.50	220.62
Heart Clontech	0	0	0.00	1.32	37.88	0.00
Hypothalamus	0	10.73	5.37	0.32	155.28	833.07
Ileum	16.49	23.89	20.19	2.58	19.38	391.28
Jejunum	82.08	38.94	60.51	6.60	7.58	458.41
Kidney	39.06	10.72	24.89	2.12	23.58	587.03
Liver	41.23	28.71	34.97	1.50	33.33	1165.67
Fetal Liver Clontech	100.26	139.8	120.03	10.40	4.81	577.07
Lung	4.2	0	2.10	2.57	19.46	40.86
Mammary Gland Clontech	75.84	122.26	99.05	13.00	3.85	380.96
Myometrium	15.76	59.25	37.51	2.34	21.37	801.39
Omentum	35.05	66.71	50.88	3.94	12.69	645.69
Ovary	96.27	189.21	142.74	4.34	11.52	1644.47
Pancreas	4.98	0	2.49	0.81	61.80	153.89
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	13.16	107.03	60.10	5.48	9.12	548.31
Placenta Clontech	0	0	0.00	5.26	9.51	0.00
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	27.68	15.44	21.56	1.23	40.65	876.42
Salivary Gland Clontech	31.31	47.7	39.51	7.31	6.84	270.21
Skeletal Muscle Clontech	0	8.62	4.31	1.26	39.68	171.03
Skin	23.3	4.31	13.81	1.21	41.32	570.45
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	30.6	0	15.30	4.92	10.16	155.49
Stomach	22.74	37.71	30.23	2.73	18.32	553.57
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	437.25	466.27	451.76	9.89	5.06	2283.92
Thyroid	29.73	11.51	20.62	2.77	18.05	372.20
Trachea Clontech	32.38	84.84	58.61	9.71	5.15	301.80
Urinary Bladder	49.96	72.21	61.09	5.47	9.14	558.36
Uterus	138.38	160.37	149.38	5.34	9.36	1398.64

Sample sbg506454MPG-1	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	2762.2	5524.40	colon normal	
colon tumor GW98-166	21940	4187.4	8374.80	colon tumor	1.52
colon normal GW98-178	22080	304.95	609.90	colon normal	
colon tumor GW98-177	22060	591.09	1182.18	colon tumor	1.94
colon normal GW98-561	23514	1334.04	2668.08	colon normal	
colon tumor GW98-560	23513	773.62	1547.24	colon tumor	-1.72
colon normal GW98-894	24691	5252.81	10505.62	colon normal	

colon tumor GW98-893	24690	1582.61	3165.22	colon tumor	-3.32
lung normal GW98-3	20742	5609.71	11219.42	lung normal	
lung tumor GW98-2	20741	244.73	489.46	lung tumor	-22.92
lung normal GW97-179	20677	5225.63	10451.26	lung normal	
lung tumor GW97-178	20676	3397.1	6794.20	lung tumor	-1.54
lung normal GW98-165	21922	4925.8	9851.60	lung normal	
lung tumor GW98-164	21921	3628.09	7256.18	lung tumor	-1.36
lung normal GW98-282	22584	1689.76	3379.52	lung normal	
lung tumor GW98-281	22583	2126.38	4252.76	lung tumor	1.26
breast normal GW00-392	28750	919.61	919.61	breast normal	
breast tumor GW00-391	28746	844.85	1689.70	breast tumor	1.84
breast normal GW00-413	28798	402.44	402.44	breast normal	
breast tumor GW00-412	28797	4379.69	8759.38	breast tumor	21.77
breast normal GW00-235:238	27592-95	59.61	59.61	breast normal	
breast tumor GW00-231:234	27588-91	182.62	182.62	breast tumor	3.06
breast normal GW98-621	23656	1437.56	2875.12	breast normal	
breast tumor GW98-620	23655	1973.41	3946.82	breast tumor	1.37
brain normal BB99-542	25507	151.01	302.02	brain normal	
brain normal BB99-406	25509	220.06	440.12	brain normal	
brain normal BB99-904	25546	118	236.00	brain normal	
brain stage 5 ALZ BB99-874	25502	37.44	74.88	brain stage 5 ALZ	-4.35
brain stage 5 ALZ BB99-887	25503	475.99	951.98	brain stage 5 ALZ	2.92
brain stage 5 ALZ BB99-862	25504	175.26	350.52	brain stage 5 ALZ	1.08
brain stage 5 ALZ BB99-927	25542	127.66	255.32	brain stage 5 ALZ	-1.28
CT lung KC	normal	2040.92	4081.84	CT lung	
lung 26 KC	normal	304.9	304.90	lung 26	
lung 27 KC	normal	97.51	97.51	lung 27	
lung 24 KC	COPD	179.61	179.61	lung 24	-6.45
lung 28 KC	COPD	345.33	345.33	lung 28	-3.35
lung 23 KC	COPD	181.29	181.29	lung 23	-6.39
lung 25 KC	normal	147.65	147.65	lung 25	
asthmatic lung ODO3112	29321	299.26	299.26	asthmatic lung	-3.87
asthmatic lung ODO3433	29323	6700	13400.00	asthmatic lung	11.57
asthmatic lung ODO3397	29322	10865.43	21730.86	asthmatic lung	18.77
asthmatic lung ODO4928	29325	5532.73	11065.46	asthmatic lung	9.56
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	4533.27	9066.54	heart	
heart ( T-1 ) ischemic	29417	996.35	1992.70	heart T-1	-4.55
heart (T-14) non-obstructive DCM	29422	787.37	1574.74	heart T-14	-5.76
heart (T-3399) DCM	29426	1496.18	2992.36	heart T-3399	-3.03

adenoid GW99-269	26162	7988.69	15977.38	adenoid	
tonsil GW98-280	22582	9400.6	18801.20	tonsil	
T cells PC00314	28453	1806.51	3613.02	T cells	
PBMNC KC		1206.11	1206.11	PBMNC	
monocyte KC		2460.19	4920.38	monocyte	
B cells PC00665	28455	24529.33	49058.66	B cells	
dendritic cells 28441		57867.91	115735.82	dendritic cells	
neutrophils	28440	34334.73	34334.73	neutrophils	
eosinophils	28446	7309.05	14618.10	eosinophils	
BM unstim KC		592.73	592.73	BM unstim	
BM stim KC		2305.64	2305.64	BM stim	3.89
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		3.91	9.78	chondrocytes	
OA Synovium IP12/01	29462	4075.04	4075.04	OA Synovium	
OA Synovium NP10/01	29461	3058.76	6117.52	OA Synovium	
OA Synovium NP57/00	28464	10311.73	20623.46	OA Synovium	
RA Synovium NP03/01	28466	15610.63	31221.26	RA Synovium	
RA Synovium NP71/00	28467	16336.72	32673.44	RA Synovium	
RA Synovium NP45/00	28475	25648.1	51296.20	RA Synovium	
OA bone (biobank)	29217	2045.31	2045.31	OA bone (biobank)	
OA bone Sample 1	J. Emory	8940.89	17881.78	OA bone	
OA bone Sample 2	J. Emory	10348.45	20696.90	OA bone	
Cartilage (pool)	Normal	4762.29	9524.58	Cartilage (pool)	
Cartilage (pool)	OA	2412.92	4825.84	Cartilage (pool)	-1.97
PBL uninfected	28441	3559.78	7119.56	PBL uninfected	
PBL HIV IIIB	28442	10815.58	21631.16	PBL HIV IIIB	3.04
MRC5 uninfected (100%)	29158	72.21	144.42	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	133.55	267.10	MRC5 HSV strain F	1.85
W12 cells	29179	6.74	13.48	W12 cells	
Keratinocytes	29180	3.55	7.10	Keratinocytes	

Gene Name sbg506454MPG-1

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.52
colon tumor	1.94
colon tumor	-1.72
colon tumor	-3.32
lung tumor	-22.92
lung tumor	-1.54

lung tumor	-1.36
lung tumor	1.26
breast tumor	1.84
breast tumor	21.77
breast tumor	3.06
breast tumor	1.37
brain stage 5 ALZ	-4.35
brain stage 5 ALZ	2.92
brain stage 5 ALZ	1.08
brain stage 5 ALZ	-1.28
lung 24	-6.45
lung 28	-3.35
lung 23	-6.39
asthmatic lung	-3.87
asthmatic lung	11.57
asthmatic lung	18.77
asthmatic lung	9.56
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-4.55
heart T-14	-5.76
heart T-3399	-3.03
BM stim	3.89
osteo dif	0.00
Cartilage (pool)	-1.97
PBL HTV IIIB	3.04
MRC5 HSV strain F	1.85

**Gene Name sbg659837OBCAM**

Highest in brain but not changed in alzheimers. Significantly increased expression in one tumor each of colon and lung sufficient to claim colon and lung cancer.

- 5 Upregulated expression in ischemic and non-obstructive DCM suggesting possible roles in these diseases

Sample sbg659837OBCAM	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	1.15	5.28	3.22	3.06	16.34	52.53
Subcutaneous Adipose Zenbio	5.25	5.54	5.40	0.96	52.36	282.46
Adrenal Gland Clontech	0	0.47	0.24	0.61	81.97	19.26
Whole Brain Clontech	7004	8885.24	7944.62	7.24	6.91	54866.16
Fetal Brain Clontech	63.3	31.88	47.59	0.48	103.95	4946.99
Cerebellum Clontech	113.86	99.7	106.78	2.17	23.04	2460.37

Cervix	0	0.9	0.45	2.42	20.66	9.30
Colon	9.45	0	4.73	2.71	18.45	87.18
Endometrium	0.95	9.52	5.24	0.73	68.21	357.09
Esophagus	0.93	0.41	0.67	1.37	36.50	24.45
Heart Clontech	2.38	1.46	1.92	1.32	37.88	72.73
Hypothalamus	15.19	3.03	9.11	0.32	155.28	1414.60
Ileum	0	0.17	0.09	2.58	19.38	1.65
Jejunum	8.83	9.37	9.10	6.60	7.58	68.94
Kidney	1.88	0.13	1.01	2.12	23.58	23.70
Liver	0.5	19.09	9.80	1.50	33.33	326.50
Fetal Liver Clontech	29.24	24.47	26.86	10.40	4.81	129.11
Lung	1.59	0.57	1.08	2.57	19.46	21.01
Mammary Gland Clontech	18.83	15.4	17.12	13.00	3.85	65.83
Myometrium	1.61	0.47	1.04	2.34	21.37	22.22
Omentum	5.14	0.36	2.75	3.94	12.69	34.90
Ovary	7.55	9.8	8.68	4.34	11.52	99.94
Pancreas	0.15	0	0.08	0.81	61.80	4.64
Head of Pancreas	7.79	0	3.90	1.57	31.85	124.04
Parotid Gland	15.83	17.02	16.43	5.48	9.12	149.86
Placenta Clontech	0.11	12.02	6.07	5.26	9.51	57.65
Prostate	0.39	2.26	1.33	3.00	16.67	22.08
Rectum	2.79	0.43	1.61	1.23	40.65	65.45
Salivary Gland Clontech	0.48	4.21	2.35	7.31	6.84	16.04
Skeletal Muscle Clontech	0.4	0	0.20	1.26	39.68	7.94
Skin	8.94	0.49	4.72	1.21	41.32	194.83
Small Intestine Clontech	0.56	0.68	0.62	0.98	51.07	31.66
Spleen	0.17	9.76	4.97	4.92	10.16	50.46
Stomach	0.47	10.35	5.41	2.73	18.32	99.08
Testis Clontech	16.85	2.95	9.90	0.57	87.87	869.95
Thymus Clontech	9.87	19.27	14.57	9.89	5.06	73.66
Thyroid	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	2.61	21.88	12.25	9.71	5.15	63.05
Urinary Bladder	0.49	5.2	2.85	5.47	9.14	26.01
Uterus	15.14	10.84	12.99	5.34	9.36	121.63

Sample sbg659837OBCAM	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/5 0 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	61.2	122.40	colon normal	
colon tumor GW98-166	21940	220.5	441.00	colon tumor	3.60
colon normal GW98-178	22080	12.34	24.68	colon normal	
colon tumor GW98-177	22060	11.21	22.42	colon tumor	-1.10

colon normal GW98-561	23514	15.49	30.98	colon normal	
colon tumor GW98-560	23513	146.12	292.24	colon tumor	9.43
colon normal GW98-894	24691	7.27	14.54	colon normal	
colon tumor GW98-893	24690	20.83	41.66	colon tumor	2.87
lung normal GW98-3	20742	12.55	25.10	lung normal	
lung tumor GW98-2	20741	19.34	38.68	lung tumor	1.54
lung normal GW97-179	20677	934.94	1869.88	lung normal	
lung tumor GW97-178	20676	3.9	7.80	lung tumor	-239.73
lung normal GW98-165	21922	0.96	1.92	lung normal	
lung tumor GW98-164	21921	108.12	216.24	lung tumor	112.63
lung normal GW98-282	22584	8.25	16.50	lung normal	
lung tumor GW98-281	22583	6.21	12.42	lung tumor	-1.33
breast normal GW00-392	28750	9.43	9.43	breast normal	
breast tumor GW00-391	28746	18.02	36.04	breast tumor	3.82
breast normal GW00-413	28798	13.42	13.42	breast normal	
breast tumor GW00-412	28797	1.94	3.88	breast tumor	-3.46
breast normal GW00-235:238	27592-95	4.61	4.61	breast normal	
breast tumor GW00-231:234	27588-91	10.16	10.16	breast tumor	2.20
breast normal GW98-621	23656	18.65	37.30	breast normal	
breast tumor GW98-620	23655	13.96	27.92	breast tumor	-1.34
brain normal BB99-542	25507	812.47	1624.94	brain normal	
brain normal BB99-406	25509	231.81	463.62	brain normal	
brain normal BB99-904	25546	583.17	1166.34	brain normal	
brain stage 5 ALZ BB99-874	25502	200.73	401.46	brain stage 5 ALZ	-2.70
brain stage 5 ALZ BB99-887	25503	685.93	1371.86	brain stage 5 ALZ	1.26
brain stage 5 ALZ BB99-862	25504	585.8	1171.60	brain stage 5 ALZ	1.08
brain stage 5 ALZ BB99-927	25542	329.32	658.64	brain stage 5 ALZ	-1.65
CT lung KC	normal	17.5	35.00	CT lung	
lung 26 KC	normal	8.07	8.07	lung 26	
lung 27 KC	normal	0.3	0.30	lung 27	
lung 24 KC	COPD	0.45	0.45	lung 24	-24.09
lung 28 KC	COPD	0.22	0.22	lung 28	-49.28
lung 23 KC	COPD	0	0.00	lung 23	-10.84
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0.52	0.52	asthmatic lung	-20.85
asthmatic lung ODO3433	29323	0.7	1.40	asthmatic lung	-7.74
asthmatic lung ODO3397	29322	1.96	3.92	asthmatic lung	-2.77
asthmatic lung ODO4928	29325	6.35	12.70	asthmatic lung	1.17
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0.9	0.90	endo bFGF	0.90
heart Clontech	normal	0	0.00	heart	
heart ( T-1 ) ischemic	29417	12.89	25.78	heart T-1	25.78

heart (T-14) non-obstructive DCM	29422	12.27	24.54	heart T-14	24.54
heart (T-3399) DCM	29426	0	0.00	heart T-3399	0.00
adenoid GW99-269	26162	4.88	9.76	adenoid	
tonsil GW98-280	22582	1.13	2.26	tonsil	
T cells PC00314	28453	5.99	11.98	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		0.15	0.30	monocyte	
B cells PC00665	28455	4.62	9.24	B cells	
dendritic cells 28441		1.33	2.66	dendritic cells	
neutrophils	28440	1.86	1.86	neutrophils	
eosinophils	28446	3.76	7.52	eosinophils	
BM unstim KC		0.15	0.15	BM unstim	
BM stim KC		0.99	0.99	BM stim	6.60
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		6.09	15.23	chondrocytes	
OA Synovium IP12/01	29462	29.16	29.16	OA Synovium	
OA Synovium NP10/01	29461	7.61	15.22	OA Synovium	
OA Synovium NP57/00	28464	10.65	21.30	OA Synovium	
RA Synovium NP03/01	28466	0.84	1.68	RA Synovium	
RA Synovium NP71/00	28467	10.01	20.02	RA Synovium	
RA Synovium NP45/00	28475	3.77	7.54	RA Synovium	
OA bone (biobank)	29217	1.34	1.34	OA bone (biobank)	
OA bone Sample 1	J. Emory	13.96	27.92	OA bone	
OA bone Sample 2	J. Emory	5.82	11.64	OA bone	
Cartilage (pool)	Normal	8.9	17.80	Cartilage (pool)	
Cartilage (pool)	OA	5.88	11.76	Cartilage (pool)	-1.51
PBL uninfected	28441	37.23	74.46	PBL uninfected	
PBL HIV IIIB	28442	12.75	25.50	PBL HIV IIIB	-2.92
MRC5 uninfected (100%)	29158	1.88	3.76	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	4.71	9.42	MRC5 HSV strain F	2.51
W12 cells	29179	2.4	4.80	W12 cells	
Keratinocytes	29180	0.47	0.94	Keratinocytes	

Gene Name sbg659837OBCAM

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	3.60
colon tumor	-1.10
colon tumor	9.43
colon tumor	2.87

lung tumor	1.54
lung tumor	-239.73
lung tumor	112.63
lung tumor	-1.33
breast tumor	3.82
breast tumor	-3.46
breast tumor	2.20
breast tumor	-1.34
brain stage 5 ALZ	-2.70
brain stage 5 ALZ	1.26
brain stage 5 ALZ	1.08
brain stage 5 ALZ	-1.65
lung 24	-24.09
lung 28	-49.28
lung 23	-10.84
asthmatic lung	-20.85
asthmatic lung	-7.74
asthmatic lung	-2.77
asthmatic lung	1.17
endo VEGF	0.00
endo bFGF	0.90
heart T-1	25.78
heart T-14	24.54
heart T-3399	0.00
BM stim	6.60
osteo dif	0.00
Cartilage (pool)	-1.51
PBL HIV IIIB	-2.92
MRC5 HSV strain F	2.51

**Gene Name sbg467870CBP**

Expression in fetal liver, thymus, monocytes, adenoid, and tonsil consistent with role in I inflammation. Upregulated in 2 of 4 asthmatic lungs, expression in OA and RA synovium, chondrocyte cells and cartilage, OA bone, and RA synovia suggest involvement in asthma, osteoarthritis, and rheumatoid arthritis. Upregulated in differentiated osteoblasts and expression in OA bone suggests possible involvement in bone disease such as osteoporosis. Down-regulated expression in HSV infected lung cell line suggest possible host factor for HSV infection. Expressed in brain but not changed in alzheimers disease.

Sample sbg467870CBP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	122.51	171.63	147.07	3.06	16.34	2403.10
Subcutaneous Adipose Zenbio	1.45	13.47	7.46	0.96	52.36	390.58
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00



Whole Brain Clontech	3940.12	4641.93	4291.03	7.24	6.91	29634.15
Fetal Brain Clontech	3.53	0	1.77	0.48	103.95	183.47
Cerebellum Clontech	22.75	10.04	16.40	2.17	23.04	377.76
Cervix	29.81	35.43	32.62	2.42	20.66	673.97
Colon	28.29	54.06	41.18	2.71	18.45	759.69
Endometrium	30.56	34.68	32.62	0.73	68.21	2225.10
Esophagus	17.68	20.49	19.09	1.37	36.50	696.53
Heart Clontech	28.33	8.29	18.31	1.32	37.88	693.56
Hypothalamus	3.33	0	1.67	0.32	155.28	258.54
Ileum	61.25	51.5	56.38	2.58	19.38	1092.54
Jejunum	67.83	122.15	94.99	6.60	7.58	719.62
Kidney	16.18	62.83	39.51	2.12	23.58	931.72
Liver	18.1	47.12	32.61	1.50	33.33	1087.00
Fetal Liver Clontech	2254.06	1918.75	2086.41	10.40	4.81	10030.79
Lung	22.15	21.19	21.67	2.57	19.46	421.60
Mammary Gland Clontech	601.21	800.88	701.05	13.00	3.85	2696.33
Myometrium	111.87	92.21	102.04	2.34	21.37	2180.34
Omentum	127.05	139.02	133.04	3.94	12.69	1688.26
Ovary	101.56	83.66	92.61	4.34	11.52	1066.94
Pancreas	0	5.97	2.99	0.81	61.80	184.49
Head of Pancreas	1	6.97	3.99	1.57	31.85	126.91
Parotid Gland	73.96	99.31	86.64	5.48	9.12	790.47
Placenta Clontech	418.31	231.45	324.88	5.26	9.51	3088.21
Prostate	48.01	84.04	66.03	3.00	16.67	1100.42
Rectum	36.56	53.99	45.28	1.23	40.65	1840.45
Salivary Gland Clontech	121.88	154.83	138.36	7.31	6.84	946.34
Skeletal Muscle Clontech	21.46	0	10.73	1.26	39.68	425.79
Skin	28.31	20.63	24.47	1.21	41.32	1011.16
Small Intestine Clontech	11.03	5.84	8.44	0.98	51.07	430.80
Spleen	25.2	33.24	29.22	4.92	10.16	296.95
Stomach	31.15	51.9	41.53	2.73	18.32	760.53
Testis Clontech	0	6.47	3.24	0.57	87.87	284.27
Thymus Clontech	2456.56	2161.41	2308.99	9.89	5.06	11673.33
Thyroid	32.73	62.2	47.47	2.77	18.05	856.77
Trachea Clontech	129.76	145.42	137.59	9.71	5.15	708.50
Urinary Bladder	137.82	144.51	141.17	5.47	9.14	1290.36
Uterus	166.73	180.21	173.47	5.34	9.36	1624.25

Sample sbg467870CBP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	5005.21	10010.42	colon normal	

colon tumor GW98-166	21940	15849.6	31699.20	colon tumor	3.17
colon normal GW98-178	22080	1796.63	3593.26	colon normal	
colon tumor GW98-177	22060	2527.09	5054.18	colon tumor	1.41
colon normal GW98-561	23514	1769.84	3539.68	colon normal	
colon tumor GW98-560	23513	4004.28	8008.56	colon tumor	2.26
colon normal GW98-894	24691	2496.8	4993.60	colon normal	
colon tumor GW98-893	24690	5145.92	10291.84	colon tumor	2.06
lung normal GW98-3	20742	2177.03	4354.06	lung normal	
lung tumor GW98-2	20741	2751.54	5503.08	lung tumor	1.26
lung normal GW97-179	20677	5925.16	11850.32	lung normal	
lung tumor GW97-178	20676	5250.96	10501.92	lung tumor	-1.13
lung normal GW98-165	21922	2705.56	5411.12	lung normal	
lung tumor GW98-164	21921	10468.54	20937.08	lung tumor	3.87
lung normal GW98-282	22584	1959.86	3919.72	lung normal	
lung tumor GW98-281	22583	937.14	1874.28	lung tumor	-2.09
breast normal GW00-392	28750	4102.06	4102.06	breast normal	
breast tumor GW00-391	28746	2805.02	5610.04	breast tumor	1.37
breast normal GW00-413	28798	4564.07	4564.07	breast normal	
breast tumor GW00-412	28797	5045.72	10091.44	breast tumor	2.21
breast normal GW00-235:238	27592-95	3527.38	3527.38	breast normal	
breast tumor GW00-231:234	27588-91	4475.08	4475.08	breast tumor	1.27
breast normal GW98-621	23656	5436.38	10872.76	breast normal	
breast tumor GW98-620	23655	7555.65	15111.30	breast tumor	1.39
brain normal BB99-542	25507	4185.89	8371.78	brain normal	
brain normal BB99-406	25509	1474.43	2948.86	brain normal	
brain normal BB99-904	25546	824.95	1649.90	brain normal	
brain stage 5 ALZ BB99-874	25502	439.29	878.58	brain stage 5 ALZ	-4.92
brain stage 5 ALZ BB99-887	25503	1034.44	2068.88	brain stage 5 ALZ	-2.09
brain stage 5 ALZ BB99-862	25504	2189.42	4378.84	brain stage 5 ALZ	1.01
brain stage 5 ALZ BB99-927	25542	2009.16	4018.32	brain stage 5 ALZ	-1.08
CT lung KC	normal	2111.76	4223.52	CT lung	
lung 26 KC	normal	308.92	308.92	lung 26	
lung 27 KC	normal	11.77	11.77	lung 27	
lung 24 KC	COPD	23.05	23.05	lung 24	-49.55
lung 28 KC	COPD	217.04	217.04	lung 28	-5.26
lung 23 KC	COPD	66.62	66.62	lung 23	-17.15
lung 25 KC	normal	24.66	24.66	lung 25	
asthmatic lung ODO3112	29321	3982.98	3982.98	asthmatic lung	3.49
asthmatic lung ODO3433	29323	2535.37	5070.74	asthmatic lung	4.44
asthmatic lung ODO3397	29322	10395.55	20791.10	asthmatic lung	18.20
asthmatic lung ODO4928	29325	5044.21	10088.42	asthmatic	8.83

				lung	
endo cells KC	control	724.08	724.08	endo cells	
endo VEGF KC		607.05	607.05	endo VEGF	-1.19
endo bFGF KC		346.88	346.88	endo bFGF	-2.09
heart Clontech	normal	338.3	676.60	heart	
heart ( T-1 ) ischemic	29417	7198.62	14397.24	heart T-1	21.28
heart (T-14) non-obstructive DCM	29422	1634.96	3269.92	heart T-14	4.83
heart (T-3399) DCM	29426	8987.22	17974.44	heart T-3399	26.57
adenoid GW99-269	26162	1327.73	2655.46	adenoid	
tonsil GW98-280	22582	3389.07	6778.14	tonsil	
T cells PC00314	28453	2349.93	4699.86	T cells	
PBMNC KC		41.03	41.03	PBMNC	
monocyte KC		21.32	42.64	monocyte	
B cells PC00665	28455	1181.61	2363.22	B cells	
dendritic cells 28441		7521.93	15043.86	dendritic cells	
neutrophils	28440	248.9	248.90	neutrophils	
eosinophils	28446	874.14	1748.28	eosinophils	
BM unstim KC		142.11	142.11	BM unstim	
BM stim KC		635.4	635.40	BM stim	4.47
osteo dif KC		2464.77	2464.77	osteo dif	5.45
osteo undif KC		452.56	452.56	osteo undif	
chondrocytes		24737.56	61843.90	chondrocytes	
OA Synovium IP12/01	29462	1788.87	1788.87	OA Synovium	
OA Synovium NP10/01	29461	7842.79	15685.58	OA Synovium	
OA Synovium NP57/00	28464	11577.91	23155.82	OA Synovium	
RA Synovium NP03/01	28466	19643.98	39287.96	RA Synovium	
RA Synovium NP71/00	28467	22772.86	45545.72	RA Synovium	
RA Synovium NP45/00	28475	16068.31	32136.62	RA Synovium	
OA bone (biobank)	29217	1829.84	1829.84	OA bone (biobank)	
OA bone Sample 1	J. Emory	11770.26	23540.52	OA bone	
OA bone Sample 2	J. Emory	2525.12	5050.24	OA bone	
Cartilage (pool)	Normal	18001.36	36002.72	Cartilage (pool)	
Cartilage (pool)	OA	7463.95	14927.90	Cartilage (pool)	-2.41
PBL uninfected	28441	3136.91	6273.82	PBL uninfected	
PBL HIV IIIB	28442	2830.85	5661.70	PBL HIV IIIB	-1.11
MRC5 uninfected (100%)	29158	25933.25	51866.50	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	279.28	558.56	MRC5 HSV strain F	-92.86
W12 cells	29179	6771.87	13543.74	W12 cells	
Keratinocytes	29180	22577.2	45154.40	Keratinocytes	

Gene Name sbg467870CBP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	3.17
colon tumor	1.41
colon tumor	2.26
colon tumor	2.06
lung tumor	1.26
lung tumor	-1.13
lung tumor	3.87
lung tumor	-2.09
breast tumor	1.37
breast tumor	2.21
breast tumor	1.27
breast tumor	1.39
brain stage 5 ALZ	-4.92
brain stage 5 ALZ	-2.09
brain stage 5 ALZ	1.01
brain stage 5 ALZ	-1.08
lung 24	-49.55
lung 28	-5.26
lung 23	-17.15
asthmatic lung	3.49
asthmatic lung	4.44
asthmatic lung	18.20
asthmatic lung	8.83
endo VEGF	-1.19
endo bFGF	-2.09
heart T-1	21.28
heart T-14	4.83
heart T-3399	26.57
BM stim	4.47
osteo dif	5.45
Cartilage (pool)	-2.41
PBL HIV IIIB	-1.11
MRC5 HSV strain F	-92.86

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Gene Name sbg514112RNase

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Low expression overall. Upregulated in 4 of 4 colon adenocarcinomas, 2 of 4 lung carcinomas, and 2 of 4 breast carcinomas suggesting claim for all cancers. Expression in spleen, PHA stimulated T and B cells, dendritic cells corroborates expression RA and OA synovium suggesting involvement in RA and OA diseases. Upregulated expression in 2 of 4 asthmatic lungs suggesting role in asthma. Upregulated in ischemic heart suggests possible involvement in ischemic heart disease. Strongly upregulated expression in HSV infected cell line.

Sample sbg514112RNase	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	2.22	3	2.61	3.06	16.34	42.65
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	2.31	1.85	2.08	0.61	81.97	170.49
Whole Brain Clontech	53.95	74.45	64.20	7.24	6.91	443.37
Fetal Brain Clontech	0	1.4	0.70	0.48	103.95	72.77
Cerebellum Clontech	0.7	1.99	1.35	2.17	23.04	30.99
Cervix	10.35	8.54	9.45	2.42	20.66	195.14
Colon	2.09	0.84	1.47	2.71	18.45	27.03
Endometrium	3.8	2.54	3.17	0.73	68.21	216.23
Esophagus	3.19	3.42	3.31	1.37	36.50	120.62
Heart Clontech	5.21	1.04	3.13	1.32	37.88	118.37
Hypothalamus	0.95	0.96	0.96	0.32	155.28	148.29
Ileum	2.04	1.5	1.77	2.58	19.38	34.30
Jejunum	10.27	2.15	6.21	6.60	7.58	47.05
Kidney	2.89	1.11	2.00	2.12	23.58	47.17
Liver	20.9	19.22	20.06	1.50	33.33	668.67
Fetal Liver Clontech	1.38	18.45	9.92	10.40	4.81	47.67
Lung	2.86	1.11	1.99	2.57	19.46	38.62
Mammary Gland Clontech	1.19	1.72	1.46	13.00	3.85	5.60
Myometrium	1.48	1.95	1.72	2.34	21.37	36.65
Omentum	13.35	0.72	7.04	3.94	12.69	89.28
Ovary	10.88	17.35	14.12	4.34	11.52	162.62
Pancreas	0.66	1.29	0.98	0.81	61.80	60.26
Head of Pancreas	1.31	7.17	4.24	1.57	31.85	135.03
Parotid Gland	2.19	0	1.10	5.48	9.12	9.99
Placenta Clontech	0.68	16.07	8.38	5.26	9.51	79.61
Prostate	1.1	0.95	1.03	3.00	16.67	17.08
Rectum	1.84	4.04	2.94	1.23	40.65	119.51
Salivary Gland Clontech	1.52	0.91	1.22	7.31	6.84	8.31
Skeletal Muscle Clontech	1.79	0.91	1.35	1.26	39.68	53.57
Skin	1.19	0.86	1.03	1.21	41.32	42.36
Small Intestine Clontech	3.14	1.72	2.43	0.98	51.07	124.11
Spleen	0.9	34.95	17.93	4.92	10.16	182.16
Stomach	0.72	2.21	1.47	2.73	18.32	26.83
Testis Clontech	0.69	1.82	1.26	0.57	87.87	110.28
Thymus Clontech	1.66	17.77	9.72	9.89	5.06	49.12
Thyroid	0.71	1.47	1.09	2.77	18.05	19.68
Trachea Clontech	18.75	19.05	18.90	9.71	5.15	97.32

Urinary Bladder	29.84	1.96	15.90	5.47	9.14	145.34
Uterus	10.06	46.86	28.46	5.34	9.36	266.48

Sample sbg514112RNase	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	6.61	13.22	colon normal	
colon tumor GW98-166	21940	102.54	205.08	colon tumor	15.51
colon normal GW98-178	22080	0.47	0.94	colon normal	
colon tumor GW98-177	22060	13.57	27.14	colon tumor	28.87
colon normal GW98-561	23514	4.51	9.02	colon normal	
colon tumor GW98-560	23513	25.13	50.26	colon tumor	5.57
colon normal GW98-894	24691	0.55	1.10	colon normal	
colon tumor GW98-893	24690	23.36	46.72	colon tumor	42.47
lung normal GW98-3	20742	9.59	19.18	lung normal	
lung tumor GW98-2	20741	48.18	96.36	lung tumor	5.02
lung normal GW97-179	20677	121.59	243.18	lung normal	
lung tumor GW97-178	20676	1.08	2.16	lung tumor	-112.58
lung normal GW98-165	21922	1.7	3.40	lung normal	
lung tumor GW98-164	21921	25.45	50.90	lung tumor	14.97
lung normal GW98-282	22584	62.77	125.54	lung normal	
lung tumor GW98-281	22583	0.31	0.62	lung tumor	-202.48
breast normal GW00-392	28750	20.59	20.59	breast normal	
breast tumor GW00-391	28746	13.93	27.86	breast tumor	1.35
breast normal GW00-413	28798	6.64	6.64	breast normal	
breast tumor GW00-412	28797	21.99	43.98	breast tumor	6.62
breast normal GW00-235:238	27592-95	4.32	4.32	breast normal	
breast tumor GW00-231:234	27588-91	31.59	31.59	breast tumor	7.31
breast normal GW98-621	23656	24.05	48.10	breast normal	
breast tumor GW98-620	23655	57.33	114.66	breast tumor	2.38
brain normal BB99-542	25507	34.49	68.98	brain normal	
brain normal BB99-406	25509	15.34	30.68	brain normal	
brain normal BB99-904	25546	12.44	24.88	brain normal	
brain stage 5 ALZ BB99-874	25502	22.56	45.12	brain stage 5 ALZ	1.09
brain stage 5 ALZ BB99-887	25503	39.16	78.32	brain stage 5 ALZ	1.89
brain stage 5 ALZ BB99-862	25504	7.79	15.58	brain stage 5 ALZ	-2.66
brain stage 5 ALZ BB99-927	25542	17.31	34.62	brain stage 5 ALZ	-1.20
CT lung KC	normal	0.54	1.08	CT lung	
lung 26 KC	normal	6.44	6.44	lung 26	
lung 27 KC	normal	2.29	2.29	lung 27	
lung 24 KC	COPD	2.85	2.85	lung 24	1.12

lung 28 KC	COPD	2.33	2.33	lung 28	-1.09
lung 23 KC	COPD	1.04	1.04	lung 23	-2.44
lung 25 KC	normal	0.33	0.33	lung 25	
asthmatic lung ODO3112	29321	3.37	3.37	asthmatic lung	1.33
asthmatic lung ODO3433	29323	2.7	5.40	asthmatic lung	2.13
asthmatic lung ODO3397	29322	5.75	11.50	asthmatic lung	4.54
asthmatic lung ODO4928	29325	11.16	22.32	asthmatic lung	8.80
endo cells KC	control	26.26	26.26	endo cells	
endo VEGF KC		50.21	50.21	endo VEGF	1.91
endo bFGF KC		11.98	11.98	endo bFGF	-2.19
heart Clontech	normal	3.65	7.30	heart	
heart ( T-1 ) ischemic	29417	37.58	75.16	heart T-1	10.30
heart (T-14) non-obstructive DCM	29422	7.85	15.70	heart T-14	2.15
heart (T-3399) DCM	29426	25.01	50.02	heart T-3399	6.85
adenoid GW99-269	26162	6.35	12.70	adenoid	
tonsil GW98-280	22582	29.12	58.24	tonsil	
T cells PC00314	28453	28.13	56.26	T cells	
PBMNC KC		0.68	0.68	PBMNC	
monocyte KC		0.48	0.96	monocyte	
B cells PC00665	28455	68.51	137.02	B cells	
dendritic cells 28441		59	118.00	dendritic cells	
neutrophils	28440	0.5	0.50	neutrophils	
eosinophils	28446	0	0.00	eosinophils	
BM unstim KC		3.41	3.41	BM unstim	
BM stim KC		0.37	0.37	BM stim	-9.22
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		0.51	1.28	chondrocytes	
OA Synovium IP12/01	29462	9.81	9.81	OA Synovium	
OA Synovium NP10/01	29461	0.85	1.70	OA Synovium	
OA Synovium NP57/00	28464	30.2	60.40	OA Synovium	
RA Synovium NP03/01	28466	8.15	16.30	RA Synovium	
RA Synovium NP71/00	28467	34.68	69.36	RA Synovium	
RA Synovium NP45/00	28475	49.69	99.38	RA Synovium	
OA bone (biobank)	29217	0.63	0.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	23.54	47.08	OA bone	
OA bone Sample 2	J. Emory	37.19	74.38	OA bone	
Cartilage (pool)	Normal	20.02	40.04	Cartilage (pool)	
Cartilage (pool)	OA	6.66	13.32	Cartilage (pool)	-3.01
PBL uninfected	28441	21.95	43.90	PBL uninfected	
PBL HIV IIIB	28442	7	14.00	PBL HIV IIIB	-3.14
MRC5 uninfected (100%)	29158	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	501.82	1003.64	MRC5 HSV strain F	1003.64
W12 cells	29179	3.76	7.52	W12 cells	

Keratinocytes	29180	0.28	0.56	Keratinocytes	
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Gene Name sbg514112RNase

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	15.51
colon tumor	28.87
colon tumor	5.57
colon tumor	42.47
lung tumor	5.02
lung tumor	-112.58
lung tumor	14.97
lung tumor	-202.48
breast tumor	1.35
breast tumor	6.62
breast tumor	7.31
breast tumor	2.38
brain stage 5 ALZ	1.09
brain stage 5 ALZ	1.89
brain stage 5 ALZ	-2.66
brain stage 5 ALZ	-1.20
lung 24	1.12
lung 28	-1.09
lung 23	-2.44
asthmatic lung	1.33
asthmatic lung	2.13
asthmatic lung	4.54
asthmatic lung	8.80
endo VEGF	1.91
endo bFGF	-2.19
heart T-1	10.30
heart T-14	2.15
heart T-3399	6.85
BM stim	-9.22
osteo undif	0.00
Cartilage (pool)	-3.01
PBL HIV IIIB	-3.14
MRC5 HSV strain F	1003.64

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Gene Name sbg962274FGF-BP

Expressed in brain with highest expression in fetal tissues. Significant expression in hypothalamus and thyroid suggests claims in thyroid disease and and metabolic disease claims related to diabetes, impaired glucose tolerance, metabolic syndrome, and obesity. Upregulated expression in all three heart diseases suggests involvement in non-obstructive DCM, DCM, and ischemic heart disease. Overexpression in one of four breast tumors suggests claim for breast cancer (caveat: undetectable expression in normal adjacent may lead to exaggerated fold overexpression). Immune cell

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expression in T and B cells, dendritic cells, chondrocytes and stimulated bone marrow consistent with expression in RA and OA synovium, OA bone, and cartilage and suggests involvement in OA and RA diseases.

Sample sbg962274FGF-BP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	455.56	624.29	539.93	7.24	6.91	3728.76
Fetal Brain Clontech	164.47	320.73	242.60	0.48	103.95	25218.30
Cerebellum Clontech	99.48	123.78	111.63	2.17	23.04	2572.12
Cervix	63.34	61.46	62.40	2.42	20.66	1289.26
Colon	110.4	0	55.20	2.71	18.45	1018.45
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	0	0.00	1.32	37.88	0.00
Hypothalamus	0	58.72	29.36	0.32	155.28	4559.01
Ileum	69.65	0	34.83	2.58	19.38	674.90
Jejunum	59.87	0	29.94	6.60	7.58	226.78
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	0	0	0.00	1.50	33.33	0.00
Fetal Liver Clontech	562.37	739.81	651.09	10.40	4.81	3130.24
Lung	0	78.59	39.30	2.57	19.46	764.49
Mammary Gland Clontech	237.04	320.2	278.62	13.00	3.85	1071.62
Myometrium	91.84	179.02	135.43	2.34	21.37	2893.80
Omentum	159.45	158.28	158.87	3.94	12.69	2016.05
Ovary	70.3	0	35.15	4.34	11.52	404.95
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	230.22	319.65	274.94	5.48	9.12	2508.53
Placenta Clontech	103.93	101.53	102.73	5.26	9.51	976.52
Prostate	88.39	90.06	89.23	3.00	16.67	1487.08
Rectum	0	70.56	35.28	1.23	40.65	1434.15
Salivary Gland Clontech	218.67	151.81	185.24	7.31	6.84	1267.03
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	0	0	0.00	4.92	10.16	0.00
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	493.89	500.57	497.23	9.89	5.06	2513.80
Thyroid	237.11	201.59	219.35	2.77	18.05	3959.39
Trachea Clontech	124.53	114.49	119.51	9.71	5.15	615.40
Urinary Bladder	72.14	92.61	82.38	5.47	9.14	752.97
Uterus	0	115.86	57.93	5.34	9.36	542.42

Sample sbg962274FGF-BP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	532.51	1065.02	colon normal	
colon tumor GW98-166	21940	597.14	1194.28	colon tumor	1.12
colon normal GW98-178	22080	108.63	217.26	colon normal	
colon tumor GW98-177	22060	433.99	867.98	colon tumor	4.00
colon normal GW98-561	23514	346.17	692.34	colon normal	
colon tumor GW98-560	23513	485.16	970.32	colon tumor	1.40
colon normal GW98-894	24691	318.86	637.72	colon normal	
colon tumor GW98-893	24690	711.68	1423.36	colon tumor	2.23
lung normal GW98-3	20742	447.66	895.32	lung normal	
lung tumor GW98-2	20741	376.57	753.14	lung tumor	-1.19
lung normal GW97-179	20677	1066.58	2133.16	lung normal	
lung tumor GW97-178	20676	426.93	853.86	lung tumor	-2.50
lung normal GW98-165	21922	947.52	1895.04	lung normal	
lung tumor GW98-164	21921	539.95	1079.90	lung tumor	-1.75
lung normal GW98-282	22584	358.48	716.96	lung normal	
lung tumor GW98-281	22583	494.08	988.16	lung tumor	1.38
breast normal GW00-392	28750	293.27	293.27	breast normal	
breast tumor GW00-391	28746	556.69	1113.38	breast tumor	3.80
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	493.54	987.08	breast tumor	987.08
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	646.3	1292.60	breast normal	
breast tumor GW98-620	23655	519.35	1038.70	breast tumor	-1.24
brain normal BB99-542	25507	2558.99	5117.98	brain normal	
brain normal BB99-406	25509	1640.03	3280.06	brain normal	
brain normal BB99-904	25546	1519.52	3039.04	brain normal	
brain stage 5 ALZ BB99-874	25502	696.08	1392.16	brain stage 5 ALZ	-2.74
brain stage 5 ALZ BB99-887	25503	1796.62	3593.24	brain stage 5 ALZ	-1.06
brain stage 5 ALZ BB99-862	25504	1654.65	3309.30	brain stage 5 ALZ	-1.15
brain stage 5 ALZ BB99-927	25542	651.31	1302.62	brain stage 5 ALZ	-2.93
CT lung KC	normal	280.34	560.68	CT lung	
lung 26 KC	normal	0	0.00	lung 26	

lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-156.37
lung 28 KC	COPD	0	0.00	lung 28	-156.37
lung 23 KC	COPD	131.98	131.98	lung 23	-1.18
lung 25 KC	normal	64.81	64.81	lung 25	
asthmatic lung ODO3112	29321	35.77	35.77	asthmatic lung	-4.37
asthmatic lung ODO3433	29323	323.27	646.54	asthmatic lung	4.13
asthmatic lung ODO3397	29322	614.8	1229.60	asthmatic lung	7.86
asthmatic lung ODO4928	29325	337.93	675.86	asthmatic lung	4.32
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	103.42	206.84	heart	
heart ( T-1 ) ischemic	29417	326.36	652.72	heart T-1	3.16
heart (T-14) non-obstructive DCM	29422	799.11	1598.22	heart T-14	7.73
heart (T-3399) DCM	29426	885.7	1771.40	heart T-3399	8.56
adenoid GW99-269	26162	1005.58	2011.16	adenoid	
tonsil GW98-280	22582	979.88	1959.76	tonsil	
T cells PC00314	28453	1516.14	3032.28	T cells	
PBMNC KC		179.43	179.43	PBMNC	
monocyte KC		338.32	676.64	monocyte	
B cells PC00665	28455	550.97	1101.94	B cells	
dendritic cells 28441		619.32	1238.64	dendritic cells	
neutrophils	28440	104.25	104.25	neutrophils	
eosinophils	28446	63.57	127.14	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		981.8	981.80	BM stim	981.80
osteo dif KC		275.28	275.28	osteo dif	1.47
osteo undif KC		187.39	187.39	osteo undif	
chondrocytes		1165.74	2914.35	chondrocytes	
OA Synovium IP12/01	29462	277.86	277.86	OA Synovium	
OA Synovium NP10/01	29461	523.26	1046.52	OA Synovium	
OA Synovium NP57/00	28464	445.78	891.56	OA Synovium	
RA Synovium NP03/01	28466	604.66	1209.32	RA Synovium	
RA Synovium NP71/00	28467	567.56	1135.12	RA Synovium	
RA Synovium NP45/00	28475	466.75	933.50	RA Synovium	
OA bone (biobank)	29217	72.67	72.67	OA bone (biobank)	
OA bone Sample 1	J. Emory	321.31	642.62	OA bone	
OA bone Sample 2	J. Emory	817.43	1634.86	OA bone	
Cartilage (pool)	Normal	1280.04	2560.08	Cartilage (pool)	
Cartilage (pool)	OA	876.26	1752.52	Cartilage (pool)	-1.46
PBL uninfected	28441	1589.59	3179.18	PBL uninfected	
PBL HIV IIIB	28442	1286.53	2573.06	PBL HIV IIIB	-1.24
MRC5 uninfected (100%)	29158	578.8	1157.60	MRC5 uninfected (100%)	

MRC5 HSV strain F	29178	184.2	368.40	MRC5 HSV strain F	-3.14
W12 cells	29179	383.66	767.32	W12 cells	
Keratinocytes	29180	326.35	652.70	Keratinocytes	

Gene Name sbg962274FGF-BP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.12
colon tumor	4.00
colon tumor	1.40
colon tumor	2.23
lung tumor	-1.19
lung tumor	-2.50
lung tumor	-1.75
lung tumor	1.38
breast tumor	3.80
breast tumor	987.08
breast tumor	0.00
breast tumor	-1.24
brain stage 5 ALZ	-2.74
brain stage 5 ALZ	-1.06
brain stage 5 ALZ	-1.15
brain stage 5 ALZ	-2.93
lung 24	-156.37
lung 28	-156.37
lung 23	-1.18
asthmatic lung	-4.37
asthmatic lung	4.13
asthmatic lung	7.86
asthmatic lung	4.32
endo VEGF	0.00
endo bFGF	0.00
heart T-1	3.16
heart T-14	7.73
heart T-3399	8.56
BM stim	981.80
osteo dif	1.47
Cartilage (pool)	-1.46
PBL HIV IIIB	-1.24
MRC5 HSV strain F	-3.14

**Table V. Additional diseases based on mRNA expression in specific tissues**

<b>Tissue Expression</b>	<b>Additional Diseases</b>
Brain	Neurological and psychiatric diseases, including Alzheimers, parasupranuclear palsey, Huntington's disease, myotonic dystrophy, anorexia, depression, schizophrenia, headache, amnesias, anxiety disorders, sleep disorders, multiple sclerosis
Heart	Cardiovascular diseases, including congestive heart failure, dilated cardiomyopathy, cardiac arrhythmias, Hodgson's Disease, myocardial infarction, cardiac arrhythmias
Lung	Respiratory diseases, including asthma, Chronic Obstructive Pulmonary Disease, cystic fibrosis, acute bronchitis, adult respiratory distress syndrome
Liver	Dyslipidemia, hypercholesterolemia, hypertriglyceridemia, cirrhosis, hepatic encephalopathy, fatty hepatocirrhosis, viral and nonviral hepatitis, Type II Diabetes Mellitis, impaired glucose tolerance
Kidney	Renal diseases, including acute and chronic renal failure, acute tubular necrosis, cystinuria, Fanconi's Syndrome, glomerulonephritis, renal cell carcinoma, renovascular hypertension
Skeletal muscle	Eulenburg's Disease, hypoglycemia, obesity, tendinitis, periodic paralyses, malignant hyperthermia, paramyotonia congenita, myotonia congenita
Intestine	Gastrointestinal diseases, including Myotonia congenita, Ileus, Intestinal Obstruction, Tropical Sprue, Pseudomembranous Enterocolitis
Spleen/lymph	Lymphangiectasia, hypersplenism, angiomas, ankylosing spondylitis, Hodgkin's Disease, macroglobulinemia, malignant lymphomas, rheumatoid arthritis
Placenta	Choriocarcinoma, hydatidiform mole, placenta previa
Testis	Testicular cancer, male reproductive diseases, including low testosterone and male infertility
Pancreas	Diabetic ketoacidosis, Type 1 & 2 diabetes, obesity, impaired glucose tolerance

**What is claimed is:**

1. An isolated polypeptide selected from the group consisting of:
  - 5 (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in Table I;
  - (b) an isolated polypeptide comprising a polypeptide sequence set forth in Table I; and
  - (c) a polypeptide sequence of a gene set forth in Table I.
- 10 2. An isolated polynucleotide selected from the group consisting of:
  - (a) an isolated polynucleotide comprising a polynucleotide sequence set forth in Table I;
  - (b) an isolated polynucleotide of a gene set forth in Table I;
  - (c) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in Table I;
  - 15 (d) an isolated polynucleotide encoding a polypeptide set forth in Table I;
  - (e) a polynucleotide which is an RNA equivalent of the polynucleotide of (a) to (d);  
or a polynucleotide sequence complementary to said isolated polynucleotide.
- 20 3. An expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.
4. A process for producing a recombinant host cell which comprises the step of introducing an expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 into a cell such that the host cell, under appropriate culture conditions, produces said  
25 polypeptide.
5. A recombinant host cell produced by the process of claim 4.
6. A membrane of a recombinant host cell of claim 5 expressing said polypeptide.
- 30 7. A process for producing a polypeptide which comprises culturing a host cell of claim 5 under conditions sufficient for the production of said polypeptide and recovering said polypeptide from the culture.

## SEQUENCE LISTING

<110> SMITHKLINE BEECHAM CORPORATION  
SMITHKLINE BEECHAM p.l.c.  
GLAXO GROUP LIMITED

<120> NOVEL COMPOUNDS

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<140> TO BE ASSIGNED

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<150> 60/218,033

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

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&lt;213&gt; Homo sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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&lt;213&gt; Homo sapiens

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&lt;213&gt; Homo sapiens

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&lt;213&gt; Homo sapiens

&lt;400&gt; 18

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;213&gt; Homo sapiens

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cccgggcccc ctggcggttc ctccgggtgc ttctcagacc ccgagcagca cgcgtgcagc 180
tggcagctcc tgctgcccgc cccggaggcc gcagcgggca gcgagctggc gctgcgctgc 240
cagagcccg acggggcgcg ccaccagtgc gctaccgcg ggcattccgga gcgctgcgca 300
gcctacgccc ctgcgccgcg gcacttctgg aagcaggtgc tgggagggct gcgcaagaag 360
cggaggccct gtcacgaccc cgcgccgctc caggcccgtc tgtgcgcggg caagaagggc 420
cacggcgccg agctgcggct agtgccccgc gctccccgc ccgcacgccc caccgtcgcg 480
ggattcgcgg gggagtccaa gccccgggccc cggaaaccgg ggcggaccgc ggagcgtgcg 540
tccggcccag ccgctgggac cccgcctccc caaagcgcac cgcccaaaga aaaccctca 600
gagaggaaga ccaacgaggg caagaggaag gcggccttgg tccccaacga ggagcgacc 660
atggggaccg ggcccagccc cgacgggctg gacgggaacg cggagctcac ggagacctac 720
tgcgctgaga agtggcactc cctctgcaac ttctttgtca atttctggaa cggtga 777

```

<210> 29  
 <211> 1483  
 <212> PRT  
 <213> Homo sapiens

```

<400> 29
Met Ser His Leu Leu Ser Ala Asn Gly Arg Ala Leu Gly Arg Gly Pro
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Gly Pro Leu Glu Pro Pro Ile Ala Thr Pro Arg Arg Pro Leu Gln Glu
20          25          30
Leu Arg Arg Ala Glu Leu Val Glu Ile Ile Val Glu Thr Glu Ala Gln
35          40          45
Thr Gly Val Ser Gly Ile Asn Val Ala Gly Gly Gly Lys Glu Gly Ile
50          55          60
Phe Val Arg Glu Leu Arg Glu Asp Ser Pro Ala Ala Arg Ser Leu Ser
65          70          75          80

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Leu	Gln	Glu	Gly	Asp	Gln	Leu	Leu	Ser	Ala	Arg	Val	Phe	Phe	Glu	Asn
				85					90					95	
Phe	Lys	Tyr	Glu	Asp	Ala	Leu	Arg	Leu	Leu	Gln	Cys	Ala	Glu	Pro	Tyr
			100					105					110		
Lys	Val	Ser	Phe	Cys	Leu	Lys	Arg	Thr	Val	Pro	Thr	Gly	Asp	Leu	Ala
		115					120					125			
Leu	Arg	Pro	Gly	Thr	Val	Ser	Gly	Tyr	Glu	Ile	Lys	Gly	Pro	Arg	Ala
	130						135				140				
Lys	Val	Ala	Lys	Leu	Asn	Ile	Gln	Ser	Leu	Ser	Pro	Val	Lys	Lys	Lys
145					150					155					160
Lys	Met	Val	Pro	Gly	Ala	Leu	Gly	Val	Pro	Ala	Asp	Leu	Ala	Pro	Val
				165					170					175	
Asp	Val	Glu	Phe	Ser	Phe	Pro	Lys	Phe	Ser	Arg	Leu	Arg	Arg	Gly	Leu
			180					185					190		
Lys	Ala	Glu	Ala	Val	Lys	Gly	Pro	Val	Pro	Ala	Ala	Pro	Ala	Arg	Arg
	195						200					205			
Arg	Leu	Gln	Leu	Pro	Arg	Leu	Arg	Val	Arg	Glu	Val	Ala	Glu	Glu	Ala
	210						215				220				
Gln	Ala	Ala	Arg	Leu	Ala	Ala	Ala	Pro	Pro	Pro	Arg	Lys	Ala	Lys	
225					230					235					240
Val	Glu	Ala	Glu	Val	Ala	Ala	Gly	Ala	Arg	Phe	Thr	Ala	Pro	Gln	Val
				245					250					255	
Glu	Leu	Val	Gly	Pro	Arg	Leu	Pro	Gly	Ala	Glu	Val	Gly	Val	Pro	Gln
			260					265					270		
Val	Ser	Ala	Pro	Lys	Ala	Ala	Pro	Ser	Ala	Glu	Ala	Ala	Gly	Gly	Phe
	275						280					285			
Ala	Leu	His	Leu	Pro	Thr	Leu	Gly	Leu	Gly	Ala	Pro	Ala	Pro	Pro	Ala
	290						295				300				
Val	Glu	Ala	Pro	Ala	Val	Gly	Ile	Gln	Val	Pro	Gln	Val	Glu	Leu	Pro
305					310					315					320
Ala	Leu	Pro	Ser	Leu	Pro	Thr	Leu	Pro	Thr	Leu	Pro	Cys	Leu	Glu	Thr
				325					330					335	
Arg	Glu	Gly	Ala	Val	Ser	Val	Val	Val	Pro	Thr	Leu	Asp	Val	Ala	Ala
			340					345					350		
Pro	Thr	Val	Gly	Val	Asp	Leu	Ala	Leu	Pro	Gly	Ala	Glu	Val	Glu	Ala
	355						360					365			
Arg	Gly	Glu	Ala	Pro	Glu	Val	Ala	Leu	Lys	Met	Pro	Arg	Leu	Ser	Phe
	370						375				380				
Pro	Arg	Phe	Gly	Ala	Arg	Ala	Lys	Glu	Val	Ala	Glu	Ala	Lys	Val	Ala
385					390					395					400
Lys	Val	Ser	Pro	Glu	Ala	Arg	Val	Lys	Gly	Pro	Arg	Leu	Arg	Met	Pro
				405					410					415	
Thr	Phe	Gly	Leu	Ser	Leu	Leu	Glu	Pro	Arg	Pro	Ala	Ala	Pro	Glu	Val
			420					425					430		
Val	Glu	Ser													



545		550		555		560
Pro Glu Val Arg Leu	Pro Glu Val Gln Leu	Pro Lys Val Ser Glu Met				
	565	570			575	
Lys Leu Pro Glu Val	Ser Glu Val Ala Val	Pro Glu Val Arg Leu Pro				
	580	585			590	
Glu Val Gln Leu Pro	Lys Val Pro Glu Met	Lys Val Pro Glu Met Lys				
	595	600			605	
Leu Pro Lys Val Pro	Glu Met Lys Leu Pro	Glu Met Lys Leu Pro Glu				
	610	615			620	
Val Gln Leu Pro Lys	Val Pro Glu Met Ala Val	Pro Asp Val His Leu				
625	630	635			640	
Pro Glu Val Gln Leu	Pro Lys Val Pro Glu Met	Lys Leu Pro Glu Met				
	645	650			655	
Lys Leu Pro Glu Val	Lys Leu Pro Lys Val	Pro Glu Met Ala Val Pro				
	660	665			670	
Asp Val His Leu Pro	Glu Val Gln Leu Pro	Lys Val Pro Glu Met Lys				
	675	680			685	
Leu Pro Lys Met Pro	Glu Met Ala Val Pro	Glu Val Arg Leu Pro Glu				
	690	695			700	
Val Gln Leu Pro Lys	Val Ser Glu Met Lys	Leu Pro Lys Val Pro Glu				
705	710	715			720	
Met Ala Val Pro Asp	Val His Leu Pro Glu	Val Gln Leu Pro Lys Val				
	725	730			735	
Cys Glu Met Lys Val	Pro Asp Met Lys Leu	Pro Glu Ile Lys Leu Pro				
	740	745			750	
Lys Val Pro Glu Met	Ala Val Pro Asp Val	His Leu Pro Glu Val Gln				
	755	760			765	
Leu Pro Lys Val Ser	Glu Ile Arg Leu Pro	Glu Met Gln Val Pro Lys				
	770	775			780	
Val Pro Asp Val His	Leu Pro Lys Ala Pro	Glu Val Lys Leu Pro Arg				
785	790	795			800	
Ala Pro Glu Val Gln	Leu Lys Ala Thr Lys	Ala Glu Gln Ala Glu Gly				
	805	810			815	
Met Glu Phe Gly Phe	Lys Met Pro Lys Met	Thr Met Pro Lys Leu Gly				
	820	825			830	
Arg Ala Glu Ser Pro	Ser Arg Gly Lys Pro	Gly Glu Ala Gly Ala Glu				
	835	840			845	
Val Ser Gly Lys Leu	Val Thr Leu Pro Cys	Leu Gln Pro Glu Val Asp				
	850	855			860	
Gly Glu Ala His Val	Gly Val Pro Ser Leu	Thr Leu Pro Ser Val Glu				
865	870	875			880	
Leu Asp Leu Pro Gly	Ala Leu Gly Leu Gln	Gly Gln Val Pro Ala Ala				
	885	890			895	
Lys Met Gly Lys Gly	Glu Arg Val Glu Gly	Pro Glu Val Ala Ala Gly				
	900	905			910	
Val Arg Glu Val Gly	Phe Arg Val Pro Ser	Val Glu Ile Val Thr Pro				
	915	920			925	
Gln Leu Pro Ala Val	Glu Ile Glu Glu Gly	Arg Leu Glu Met Ile Glu				
	930	935			940	
Thr Lys Val Lys Pro	Ser Ser Lys Phe Ser	Leu Pro Lys Phe Gly Leu				
945	950	955			960	
Ser Gly Pro Lys Val	Ala Lys Ala Glu Ala	Glu Gly Ala Gly Arg Ala				
	965	970			975	
Thr Lys Leu Lys Val	Ser Lys Phe Ala Ile	Ser Leu Pro Lys Ala Arg				
	980	985			990	
Val Gly Ala Glu Ala	Glu Ala Lys Gly Ala	Gly Glu Ala Gly Leu Leu				
	995	1000			1005	
Pro Ala Leu Asp Leu	Ser Ile Pro Gln Leu	Ser Leu Asp Ala His Leu				
1010	1015	1020				

Pro Ser Gly Lys Val Glu Val Ala Gly Ala Asp Leu Lys Phe Lys Gly  
 1025 1030 1035 1040  
 Pro Arg Phe Ala Leu Pro Lys Phe Gly Val Arg Gly Arg Asp Thr Glu  
 1045 1050 1055  
 Ala Ala Glu Leu Val Pro Gly Val Ala Glu Leu Glu Gly Lys Gly Trp  
 1060 1065 1070  
 Gly Trp Asp Gly Arg Val Lys Met Pro Lys Leu Lys Met Pro Ser Phe  
 1075 1080 1085  
 Gly Leu Ala Arg Gly Lys Glu Ala Glu Val Gln Gly Asp Arg Ala Ser  
 1090 1095 1100  
 Pro Gly Glu Lys Ala Glu Ser Thr Ala Val Gln Leu Lys Ile Pro Glu  
 1105 1110 1115 1120  
 Val Glu Leu Val Thr Leu Gly Ala Gln Glu Gly Arg Ala Glu Gly  
 1125 1130 1135  
 Ala Val Ala Val Ser Gly Met Gln Leu Ser Gly Leu Lys Val Ser Thr  
 1140 1145 1150  
 Ala Gly Gln Val Val Thr Glu Gly His Asp Ala Gly Leu Arg Met Pro  
 1155 1160 1165  
 Pro Leu Gly Ile Ser Leu Pro Gln Val Glu Leu Thr Gly Phe Gly Glu  
 1170 1175 1180  
 Ala Gly Thr Pro Gly Gln Gln Ala Gln Ser Thr Val Pro Ser Ala Glu  
 1185 1190 1195 1200  
 Gly Thr Ala Gly Tyr Arg Val Gln Val Pro Gln Val Thr Leu Ser Leu  
 1205 1210 1215  
 Pro Gly Ala Gln Val Ala Gly Gly Glu Leu Leu Val Gly Glu Gly Val  
 1220 1225 1230  
 Phe Lys Met Pro Thr Val Thr Val Pro Gln Leu Glu Leu Asp Val Gly  
 1235 1240 1245  
 Leu Ser Arg Glu Ala Gln Ala Gly Glu Ala Ala Thr Gly Glu Gly Gly  
 1250 1255 1260  
 Leu Arg Leu Lys Leu Pro Thr Leu Gly Ala Arg Ala Arg Val Gly Gly  
 1265 1270 1275 1280  
 Glu Gly Ala Glu Glu Gln Pro Pro Gly Ala Glu Arg Thr Phe Cys Leu  
 1285 1290 1295  
 Ser Leu Pro Asp Val Glu Leu Ser Pro Ser Gly Gly Asn His Ala Glu  
 1300 1305 1310  
 Tyr Gln Val Ala Glu Gly Glu Gly Ala Gly His Lys Leu Lys Val  
 1315 1320 1325  
 Arg Leu Pro Arg Phe Gly Leu Val Arg Ala Lys Glu Gly Ala Glu Glu  
 1330 1335 1340  
 Gly Glu Lys Ala Lys Ser Pro Lys Leu Arg Leu Pro Arg Val Gly Phe  
 1345 1350 1355 1360  
 Ser Gln Ser Glu Met Val Thr Gly Glu Gly Ser Pro Ser Pro Glu Glu  
 1365 1370 1375  
 Glu Glu Glu Glu Glu Glu Gly Ser Gly Glu Gly Ala Ser Gly Arg  
 1380 1385 1390  
 Arg Gly Arg Val Arg Val Arg Leu Pro Arg Val Gly Leu Ala Ala Pro  
 1395 1400 1405  
 Ser Lys Ala Ser Arg Gly Gln Glu Gly Asp Ala Ala Pro Lys Ser Pro  
 1410 1415 1420  
 Val Arg Glu Lys Ser Pro Lys Phe Arg Phe Pro Arg Val Ser Leu Ser  
 1425 1430 1435 1440  
 Pro Lys Ala Arg Ser Gly Ser Gly Asp Gln Glu Glu Gly Gly Leu Arg  
 1445 1450 1455  
 Val Arg Leu Pro Ser Val Gly Phe Ser Glu Thr Gly Ala Pro Gly Pro  
 1460 1465 1470  
 Ala Arg Met Glu Gly Ala Gln Ala Ala Val  
 1475 1480

<210> 30  
 <211> 1461  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
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 Asn Val Ala Gly Gly Gly Lys Glu Gly Ile Phe Val Arg Glu Leu Arg  
 35 40 45  
 Glu Asp Ser Pro Ala Ala Arg Ser Leu Ser Leu Gln Glu Gly Asp Gln  
 50 55 60  
 Leu Leu Ser Ala Arg Val Phe Phe Glu Asn Phe Lys Tyr Glu Asp Ala  
 65 70 75 80  
 Leu Arg Leu Leu Gln Cys Ala Glu Pro Tyr Lys Val Ser Phe Cys Leu  
 85 90 95  
 Lys Arg Thr Val Pro Thr Gly Asp Leu Ala Leu Arg Pro Gly Thr Val  
 100 105 110  
 Ser Gly Tyr Glu Ile Lys Gly Pro Arg Ala Lys Val Ala Lys Leu Asn  
 115 120 125  
 Ile Gln Ser Leu Ser Pro Val Lys Lys Lys Lys Met Val Pro Gly Ala  
 130 135 140  
 Leu Gly Val Pro Ala Asp Leu Ala Pro Val Asp Val Glu Phe Ser Phe  
 145 150 155 160  
 Pro Lys Phe Ser Arg Leu Arg Arg Gly Leu Lys Ala Glu Ala Val Lys  
 165 170 175  
 Gly Pro Val Pro Ala Ala Pro Ala Arg Arg Arg Leu Gln Leu Pro Arg  
 180 185 190  
 Leu Arg Val Arg Glu Val Ala Glu Glu Ala Gln Ala Ala Arg Leu Ala  
 195 200 205  
 Ala Ala Ala Pro Pro Pro Arg Lys Ala Lys Val Glu Ala Glu Val Ala  
 210 215 220  
 Ala Gly Ala Arg Phe Thr Ala Pro Gln Val Glu Leu Val Gly Pro Arg  
 225 230 235 240  
 Leu Pro Gly Ala Glu Val Gly Val Pro Gln Val Ser Ala Pro Lys Ala  
 245 250 255  
 Ala Pro Ser Ala Glu Ala Ala Gly Gly Phe Ala Leu His Leu Pro Thr  
 260 265 270  
 Leu Gly Leu Gly Ala Pro Ala Pro Pro Ala Val Glu Ala Pro Ala Val  
 275 280 285  
 Gly Ile Gln Val Pro Gln Val Glu Leu Pro Ala Leu Pro Ser Leu Pro  
 290 295 300  
 Thr Leu Pro Thr Leu Pro Cys Leu Glu Thr Arg Glu Gly Ala Val Ser  
 305 310 315 320  
 Val Val Val Pro Thr Leu Asp Val Ala Ala Pro Thr Val Gly Val Asp  
 325 330 335  
 Leu Ala Leu Pro Gly Ala Glu Val Glu Ala Arg Gly Glu Ala Pro Glu  
 340 345 350  
 Val Ala Leu Lys Met Pro Arg Leu Ser Phe Pro Arg Phe Gly Ala Arg  
 355 360 365  
 Ala Lys Glu Val Ala Glu Ala Lys Val Ala Lys Val Ser Pro Glu Ala  
 370 375 380  
 Arg Val Lys Gly Pro Arg Leu Arg Met Pro Thr Phe Gly Leu Ser Leu  
 385 390 395 400  
 Leu Glu Pro Arg Pro Ala Ala Pro Glu Val Val Glu Ser Lys Leu Lys  
 405 410 415  
 Leu Pro Thr Ile Lys Met Pro Ser Leu Gly Ile Gly Val Ser Gly Pro

				420											
Glu	Val	Lys	Val	Pro	Lys	Gly	Pro	Glu	Val	Lys	Leu	Pro	Lys	Ala	Pro
		435					440					445			
Glu	Val	Lys	Leu	Pro	Lys	Val	Pro	Glu	Ala	Ala	Leu	Pro	Glu	Val	Arg
		450				455					460				
Leu	Pro	Glu	Val	Glu	Leu	Pro	Lys	Val	Ser	Glu	Met	Lys	Leu	Pro	Lys
465					470					475					480
Val	Pro	Glu	Met	Ala	Val	Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Glu	Leu
			485						490					495	
Pro	Lys	Val	Ser	Glu	Met	Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val
		500						505				510			
Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Gln	Leu	Leu	Lys	Val	Ser	Glu	Met
		515					520					525			
Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val	Pro	Glu	Val	Arg	Leu	Pro
		530				535					540				
Glu	Val	Gln	Leu	Pro	Lys	Val	Ser	Glu	Met	Lys	Leu	Pro	Glu	Val	Ser
545					550					555					560
Glu	Val	Ala	Val	Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Gln	Leu	Pro	Lys
			565						570					575	
Val	Pro	Glu	Met	Lys	Val	Pro	Glu	Met	Lys	Leu	Pro	Lys	Val	Pro	Glu
			580					585				590			
Met	Lys	Leu	Pro	Glu	Met	Lys	Leu	Pro	Glu	Val	Gln	Leu	Pro	Lys	Val
		595					600					605			
Pro	Glu	Met	Ala	Val	Pro	Asp	Val	His	Leu	Pro	Glu	Val	Gln	Leu	Pro
		610				615					620				
Lys	Val	Pro	Glu	Met	Lys	Leu	Pro	Glu	Met	Lys	Leu	Pro	Glu	Val	Lys
625					630					635					640
Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val	Pro	Asp	Val	His	Leu	Pro	Glu
			645						650					655	
Val	Gln	Leu	Pro	Lys	Val	Pro	Glu	Met	Lys	Leu	Pro	Lys	Met	Pro	Glu
			660					665				670			
Met	Ala	Val	Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Gln	Leu	Pro	Lys	Val
		675					680					685			
Ser	Glu	Met	Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val	Pro	Asp	Val
		690				695					700				
His	Leu	Pro	Glu	Val	Gln	Leu	Pro	Lys	Val	Cys	Glu	Met	Lys	Val	Pro
705					710					715					720
Asp	Met	Lys	Leu	Pro	Glu	Ile	Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala
			725						730					735	
Val	Pro	Asp	Val	His	Leu	Pro	Glu	Val	Gln	Leu	Pro	Lys	Val	Ser	Glu
			740					745				750			
Ile	Arg	Leu	Pro	Glu	Met	Gln	Val	Pro	Lys	Val	Pro	Asp	Val	His	Leu
		755				760						765			
Pro	Lys	Ala	Pro	Glu	Val	Lys	Leu	Pro	Arg	Ala	Pro	Glu	Val	Gln	Leu
		770				775					780				

Arg Val Pro Ser Val Glu Ile Val Thr Pro Gln Leu Pro Ala Val Glu  
 900 905 910  
 Ile Glu Glu Gly Arg Leu Glu Met Ile Glu Thr Lys Val Lys Pro Ser  
 915 920 925  
 Ser Lys Phe Ser Leu Pro Lys Phe Gly Leu Ser Gly Pro Lys Val Ala  
 930 935 940  
 Lys Ala Glu Ala Glu Gly Ala Gly Arg Ala Thr Lys Leu Lys Val Ser  
 945 950 955 960  
 Lys Phe Ala Ile Ser Leu Pro Lys Ala Arg Val Gly Ala Glu Ala Glu  
 965 970 975  
 Ala Lys Gly Ala Gly Glu Ala Gly Leu Leu Pro Ala Leu Asp Leu Ser  
 980 985 990  
 Ile Pro Gln Leu Ser Leu Asp Ala His Leu Pro Ser Gly Lys Val Glu  
 995 1000 1005  
 Val Ala Gly Ala Asp Leu Lys Phe Lys Gly Pro Arg Phe Ala Leu Pro  
 1010 1015 1020  
 Lys Phe Gly Val Arg Gly Arg Asp Thr Glu Ala Ala Glu Leu Val Pro  
 1025 1030 1035 1040  
 Gly Val Ala Glu Leu Glu Gly Lys Gly Trp Gly Trp Asp Gly Arg Val  
 1045 1050 1055  
 Lys Met Pro Lys Leu Lys Met Pro Ser Phe Gly Leu Ala Arg Gly Lys  
 1060 1065 1070  
 Glu Ala Glu Val Gln Gly Asp Arg Ala Ser Pro Gly Glu Lys Ala Glu  
 1075 1080 1085  
 Ser Thr Ala Val Gln Leu Lys Ile Pro Glu Val Glu Leu Val Thr Leu  
 1090 1095 1100  
 Gly Ala Gln Glu Glu Gly Arg Ala Glu Gly Ala Val Ala Val Ser Gly  
 1105 1110 1115 1120  
 Met Gln Leu Ser Gly Leu Lys Val Ser Thr Ala Gly Gln Val Val Thr  
 1125 1130 1135  
 Glu Gly His Asp Ala Gly Leu Arg Met Pro Pro Leu Gly Ile Ser Leu  
 1140 1145 1150  
 Pro Gln Val Glu Leu Thr Gly Phe Gly Glu Ala Gly Thr Pro Gly Gln  
 1155 1160 1165  
 Gln Ala Gln Ser Thr Val Pro Ser Ala Glu Gly Thr Ala Gly Tyr Arg  
 1170 1175 1180  
 Val Gln Val Pro Gln Val Thr Leu Ser Leu Pro Gly Ala Gln Val Ala  
 1185 1190 1195 1200  
 Gly Gly Glu Leu Leu Val Gly Glu Gly Val Phe Lys Met Pro Thr Val  
 1205 1210 1215  
 Thr Val Pro Gln Leu Glu Leu Asp Val Gly Leu Ser Arg Glu Ala Gln  
 1220 1225 1230  
 Ala Gly Glu Ala Ala Thr Gly Glu Gly Gly Leu Arg Leu Lys Leu Pro  
 1235 1240 1245  
 Thr Leu Gly Ala Arg Ala Arg Val Gly Gly Glu Gly Ala Glu Glu Gln  
 1250 1255 1260  
 Pro Pro Gly Ala Glu Arg Thr Phe Cys Leu Ser Leu Pro Asp Val Glu  
 1265 1270 1275 1280  
 Leu Ser Pro Ser Gly Gly Asn His Ala Glu Tyr Gln Val Ala Glu Gly  
 1285 1290 1295  
 Glu Gly Glu Ala Gly His Lys Leu Lys Val Arg Leu Pro Arg Phe Gly  
 1300 1305 1310  
 Leu Val Arg Ala Lys Glu Gly Ala Glu Glu Gly Glu Lys Ala Lys Ser  
 1315 1320 1325  
 Pro Lys Leu Arg Leu Pro Arg Val Gly Phe Ser Gln Ser Glu Met Val  
 1330 1335 1340  
 Thr Gly Glu Gly Ser Pro Ser Pro Glu Glu Glu Glu Glu Glu Glu  
 1345 1350 1355 1360  
 Glu Gly Ser Gly Glu Gly Ala Ser Gly Arg Arg Gly Arg Val Arg Val

[illegible]

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<210> 31
<211> 491
<212> PRT
<213> Homo sapiens
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Met 1	Gln	Pro	Thr	Gly 5	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	Tyr	
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			20					25					30			
Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	Leu	Ser	Thr	
		35					40					45				
Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	Pro	Ser	Ala	Leu	
	50					55					60					
Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	Lys	Thr	Leu	Asp	Leu	
65					70						75				80	
Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	Phe	Pro	Leu	Val	Asp	Gly	
				85					90					95		
His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	Gln	Arg	Tyr	Lys	Asn	Val	Leu	
			100					105					110			
Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	
		115					120					125				
Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	Ala	Gln	Val	Pro	Gln	Gly	His	Thr	
						135					140					
Gly	Cys	His	Ser	Met	Ala	Ala	Gly	Gly	Cys	Trp	Gly	His	Arg	Asn	Leu	
145				150					155					160		
Gly	Ser	Gln	Asp	Val	Thr	Leu	Glu	Val	Leu	Phe	Leu	Gly	Ser	Asn	His	
				165					170					175		
Leu	Thr	Leu	Tyr	Leu	Leu	Leu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	
			180					185					190			
Cys	Leu	Ile	Gly	Val	Glu	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	
		195					200					205				
Val	Leu	Arg	Ser	Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	
	210					215					220					
Phe	Thr	Cys	Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	
225					230					235				240		
His	Met	Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	
				245					250					255		
Val	Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	
			260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	
		275					280					285				
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu	Leu	Asn	
	290					295					300					
Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	Ile	Val	

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305          310          315          320
Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu Leu Ala Asn
          325          330          335
Val Ser Thr Val Ala Asp Asp Ser Asn Arg Cys Ser Val Pro Val Ile
          340          345          350
Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp Gly Thr Gly Arg
          355          360          365
Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr Pro Val Leu Ile Glu
          370          375          380
Glu Leu Leu Ser Arg Ser Trp Ser Glu Glu Glu Leu Gln Gly Val Leu
385          390          395          400
Arg Gly Asn Leu Leu Arg Val Phe Arg Gln Val Glu Lys Val Arg Glu
          405          410          415
Glu Ser Arg Ala Gln Ser Pro Val Glu Ala Glu Phe Pro Tyr Gly Gln
          420          425          430
Leu Ser Thr Ser Cys His Ser His Leu Val Pro Gln Asn Gly His Gln
          435          440          445
Ala Thr His Leu Glu Val Thr Lys Gln Pro Thr Asn Arg Val Pro Trp
450          455          460
Arg Ser Ser Asn Ala Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala
465          470          475          480
Ala Thr Ile Pro Thr Phe Thr Gln Trp Leu Cys
          485          490

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&lt;210&gt; 32

&lt;211&gt; 489

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

```

Ala Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
1          5          10          15
Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg Gln
          20          25          30
Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala Leu Ser
          35          40          45
Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val Pro Ser Ala
50          55          60
Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro Lys Thr Leu Asp
65          70          75          80
Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser Phe Pro Leu Val Asp
          85          90          95
Gly His Asn Asp Leu Pro Gln Val Leu Arg Gln Arg Tyr Lys Asn Val
          100          105          110
Leu Gln Asp Val Asn Leu Arg Asn Phe Ser His Gly Gln Thr Ser Leu
          115          120          125
Asp Arg Leu Arg Asp Gly Leu Val Gly Ala Gln Phe Trp Ser Ala Ser
          130          135          140
Val Ser Cys Gln Ser Gln Asp Gln Thr Ala Val Arg Leu Ala Leu Glu
145          150          155          160
Gln Ile Asp Leu Ile His Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu
          165          170          175
Leu Val Thr Ser Ala Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys
          180          185          190
Leu Ile Gly Val Glu Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val
          195          200          205
Leu Arg Ser Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe
210          215          220
Thr Cys Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His

```

225 230 235 240  
 Met Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val  
 245 250 255  
 Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala Ser  
 260 265 270  
 Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro Val Ile  
 275 280 285  
 Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu Leu Asn Val  
 290 295 300  
 Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly Ile Val Met  
 305 310 315 320  
 Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu Leu Ala Asn Val  
 325 330 335  
 Ser Thr Val Ala Asp His Phe Asp His Ile Lys Ala Val Ile Gly Ser  
 340 345 350  
 Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp Gly Ala Gly Lys Phe Pro  
 355 360 365  
 Gln Gly Leu Glu Asp Val Ser Thr Tyr Pro Val Leu Ile Glu Glu Leu  
 370 375 380  
 Leu Ser Arg Ser Trp Ser Glu Glu Glu Leu Gln Gly Val Leu Arg Gly  
 385 390 395 400  
 Asn Leu Leu Arg Val Phe Arg Gln Val Glu Lys Val Arg Glu Glu Ser  
 405 410 415  
 Arg Ala Gln Ser Pro Val Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser  
 420 425 430  
 Thr Ser Cys His Ser His Leu Val Pro Gln Asn Gly His Gln Ala Thr  
 435 440 445  
 His Leu Glu Val Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser  
 450 455 460  
 Ser Asn Ala Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr  
 465 470 475 480  
 Ile Pro Thr Phe Thr Gln Trp Leu Cys  
 485

<210> 33  
 <211> 514  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
 Asx Met Ile Arg Thr Pro Leu Ser Ala Ser Ala His Arg Leu Leu Leu  
 1 5 10 15  
 Pro Gly Ser Arg Gly Arg Pro Pro Arg Asn Met Gln Pro Thr Gly Arg  
 20 25 30  
 Glu Gly Ser Arg Ala Leu Ser Arg Arg Tyr Leu Arg Arg Leu Leu Leu  
 35 40 45  
 Leu Leu Leu Leu Leu Leu Leu Arg Gln Pro Val Thr Arg Ala Glu Thr  
 50 55 60  
 Thr Pro Gly Ala Pro Arg Ala Leu Ser Thr Leu Gly Ser Pro Ser Leu  
 65 70 75 80  
 Phe Thr Thr Pro Gly Val Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr  
 85 90 95  
 Thr Pro Gly Thr Pro Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala  
 100 105 110  
 Leu Met Arg Ser Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln  
 115 120 125  
 Val Leu Arg Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg  
 130 135 140  
 Asn Phe Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu



145		150		155		160
Val Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp						
	165		170		175	
Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His Arg						
	180		185		190	
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Glu Gly						
	195		200		205	
Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly						
	210		215		220	
His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser Phe Tyr Val Leu						
	225		230		235	
Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys Ser Thr Pro Trp Ala						
	245		250		255	
Glu Ser Ser Thr Lys Phe Arg His His Met Tyr Thr Asn Val Ser Gly						
	260		265		270	
Leu Thr Ser Phe Gly Glu Lys Val Val Glu Glu Leu Asn Arg Leu Gly						
	275		280		285	
Met Met Ile Asp Leu Ser Tyr Ala Ser Asp Thr Leu Ile Arg Arg Val						
	290		295		300	
Leu Glu Val Ser Gln Ala Pro Val Ile Phe Ser His Ser Ala Ala Arg						
	305		310		315	
Ala Val Cys Asp Asn Leu Leu Asn Val Pro Asp Asp Ile Leu Gln Leu						
	325		330		335	
Leu Lys Lys Asn Gly Gly Ile Val Met Val Thr Leu Ser Met Gly Val						
	340		345		350	
Leu Gln Cys Asn Leu Leu Ala Asn Val Ser Thr Val Ala Asp His Phe						
	355		360		365	
Asp His Ile Lys Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly						
	370		375		380	
Asp Tyr Asp Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser						
	385		390		395	
Thr Tyr Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Ser Trp Ser Glu						
	405		410		415	
Glu Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg						
	420		425		430	
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val Glu						
	435		440		445	
Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser His Leu						
	450		455		460	
Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val Thr Lys Gln						
	465		470		475	
Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala Ser Pro Tyr Leu						
	485		490		495	
Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro Thr Phe Thr Gln Trp						
	500		505		510	
Leu Cys						

<210> 34  
 <211> 512  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala Ser Ala Pro Val  
 1 5 10 15  
 Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala Pro Gln Asn Val  
 20 25 30  
 Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val Thr Trp Asp Pro

	35					40					45				
Pro 60	Pro 50	Pro	Glu	Ser	Gln	Asn 55	Gly	Asn	Ile	Gln	Gly 60	Tyr	Lys	Ala	Arg
Pro 65	Ser	Arg	Ala	Ile	Tyr 70	Tyr	Trp	Glu	Ala	Asp 75	Ser	Gln	Asn	Glu	Thr 80
Glu	Lys	Met	Lys	Val 85	Leu	Phe	Leu	Pro 90	Glu	Pro	Val	Val	Arg	Leu 95	Lys
Asn	Leu	Thr	Ser 100	His	Thr	Lys	Tyr	Leu 105	Val	Ser	Ile	Ser	Ala 110	Phe	Asn
Ala	Ala	Gly 115	Asp	Gly	Pro	Lys	Ser 120	Asp	Pro	Gln	Gln	Gly 125	Arg	Thr	His
Gln	Ala	Ala 130	Pro	Gly	Ala	Pro 135	Ser	Phe	Leu	Ala	Phe 140	Ser	Glu	Ile	Thr
Ser 145	Thr	Thr	Leu	Asn 150	Val	Ser	Trp	Gly	Glu	Pro 155	Ala	Ala	Ala	Asn	Gly 160
Ile	Leu	Gln	Gly	Tyr 165	Arg	Val	Val	Tyr	Glu	Pro 170	Leu	Ala	Pro	Val	Gln 175
Gly	Val	Ser	Lys 180	Val	Val	Thr	Val	Glu 185	Val	Arg	Gly	Asn	Trp 190	Gln	Arg
Trp	Leu	Lys 195	Val	Arg	Asp	Leu	Thr 200	Lys	Gly	Val	Thr	Tyr	Phe 205	Phe	Arg
Val	Gln	Ala 210	Arg	Thr	Ile	Thr 215	Tyr	Gly	Pro	Glu	Leu 220	Gln	Ala	Asn	Ile
Thr 225	Ala	Gly	Pro	Ala	Glu 230	Gly	Ser	Pro	Gly	Ser 235	Pro	Arg	Asp	Val	Leu 240
Val	Thr	Lys	Ser	Ala 245	Ser	Glu	Leu	Thr 250	Leu	Gln	Trp	Thr	Glu	Gly 255	His
Ser	Gly	Asp 260	Thr	Pro	Thr	Thr	Gly 265	Tyr	Val	Ile	Glu	Ala	Arg 270	Pro	Ser
Asp	Glu	Gly 275	Leu	Trp	Asp	Met	Phe 280	Val	Lys	Asp	Ile	Pro 285	Arg	Ser	Ala
Thr	Ser 290	Tyr	Thr	Leu	Ser	Leu 295	Asp	Lys	Leu	Arg	Gln 300	Gly	Val	Thr	Tyr
Glu 305	Phe	Arg	Val	Val	Ala 310	Val	Asn	Glu	Ala	Gly 315	Tyr	Gly	Glu	Pro	Ser 320
Asn	Pro	Ser	Thr	Ala 325	Val	Ser	Ala	Gln	Val	Glu 330	Ala	Pro	Phe	Tyr	Glu 335
Glu	Trp	Trp	Phe 340	Leu	Leu	Val	Met	Ala 345	Leu	Ser	Ser	Leu	Ile	Val	Ile 350
Leu	Leu	Val 355	Val	Phe	Ala	Leu	Val 360	Leu	His	Gly	Gln	Asn	Lys 365	Lys	Tyr
Lys	Asn 370	Cys	Ser	Thr	Gly	Ala 375	Gly	Lys	Gly	Ile	Ser 380	Thr	Met	Glu	Glu
Ser 385	Val	Thr	Leu	Asp	Asn 390	Gly	Gly	Phe	Ala	Ala 395	Leu	Glu	Leu	Ser	Ser 400
Arg	His	Leu	Asn 405	Val	Lys	Ser	Thr	Phe	Ser	Lys 410	Lys	Asn	Gly	Thr	Ser 415
Met	Gly	Pro	His 420	Pro	Arg	Ser	Pro	Pro	Arg	Pro 425	Ser	Pro	Gly	Gly	Leu
His	Tyr 435	Ser	Asp	Glu	Asp	Ile	Cys 440	Asn	Lys	Tyr	Asn	Gly 445	Ala	Val	Leu
Thr	Glu 450	Ser	Val	Ser	Leu	Lys 455	Glu	Lys	Ser	Ala	Asp 460	Ala	Ser	Glu	Ser
Glu 465	Val	Ser	Val	Gly	Ala 470	Tyr	Phe	Arg	Ala	Val 475	Thr	Ile	Ser	Pro	Tyr 480
Phe	Cys	Lys	Asp	Ala 485	Gly	Phe	Ala	Val	Arg	Thr 490	Ile	Ala	Leu	Gly	Leu 495
Ala	Glu	Thr	Ala 500	Gly	Ser	Lys	Ala	Asp 505	Ala	Arg	Lys	Gly	Thr	Phe	Val

<210> 35  
 <211> 1152  
 <212> PRT  
 <213> Homo sapiens

<400> 35  
 Ala Met Leu Ser Met Leu Ala Ala Gly Leu Leu Cys Val Pro Trp Val  
 1 5 10 15  
 Pro Gln Ser His Thr Ala Thr Arg Asn Gln Ser Leu Leu Val Met Gly  
 20 25 30  
 Leu Gln Arg Ser Pro Lys Met Ser Ser Arg Ala Leu Leu Val Gly Ala  
 35 40 45  
 Ile Gly Asp Glu Glu Glu Trp Val Thr Leu Tyr Glu Glu Glu Asn Glu  
 50 55 60  
 Pro Asp Ala Gln Met Leu Glu Ile Pro Asn Leu Thr Pro Tyr Thr His  
 65 70 75 80  
 Tyr Arg Phe Arg Met Lys Gln Val Asn Ile Val Gly Pro Ser Pro Tyr  
 85 90 95  
 Ser Pro Ser Ser Arg Val Ile Gln Thr Leu Gln Ala Pro Pro Asp Val  
 100 105 110  
 Ala Pro Thr Ser Val Thr Val Arg Thr Ala Ser Glu Thr Ser Leu Arg  
 115 120 125  
 Leu Arg Trp Val Pro Leu Pro Asp Ser Gln Tyr Asn Gly Asn Pro Glu  
 130 135 140  
 Ser Val Gly Tyr Arg Ile Lys Tyr Trp Arg Ser Asp Leu Gln Ser Ser  
 145 150 155 160  
 Ala Val Ala Gln Val Val Ser Asp Arg Leu Glu Arg Glu Phe Thr Ile  
 165 170 175  
 Glu Glu Leu Glu Glu Trp Met Glu Tyr Glu Leu Gln Met Gln Ala Phe  
 180 185 190  
 Asn Ala Val Gly Ala Gly Pro Trp Ser Glu Val Val Arg Gly Arg Thr  
 195 200 205  
 Arg Glu Ser Val Pro Ser Ala Ala Pro Glu Asn Val Ser Ala Glu Ala  
 210 215 220  
 Val Ser Ser Thr Gln Ile Leu Leu Thr Trp Thr Ser Val Pro Glu Gln  
 225 230 235 240  
 Asp Gln Asn Gly Leu Ile Leu Gly Tyr Lys Ile Leu Phe Arg Ala Lys  
 245 250 255  
 Asp Leu Asp Pro Glu Pro Arg Ser His Ile Val Arg Gly Asn His Thr  
 260 265 270  
 Gln Ser Ala Leu Leu Ala Gly Leu Arg Lys Phe Val Leu Tyr Glu Leu  
 275 280 285  
 Gln Val Leu Ala Phe Thr Arg Ile Gly Asn Gly Val Pro Ser Thr Pro  
 290 295 300  
 Leu Ile Leu Glu Arg Thr Lys Asp Asp Ala Pro Gly Pro Pro Val Arg  
 305 310 315 320  
 Leu Val Phe Pro Glu Val Arg Leu Thr Ser Val Arg Ile Val Trp Gln  
 325 330 335  
 Pro Pro Glu Glu Pro Asn Gly Ile Ile Leu Gly Tyr Gln Ile Ala Tyr  
 340 345 350  
 Arg Leu Ala Ser Ser Ser Pro His Thr Phe Thr Thr Val Glu Val Gly  
 355 360 365  
 Ala Thr Val Arg Gln Phe Thr Ala Thr Asp Leu Ala Pro Glu Ser Ala  
 370 375 380  
 Tyr Ile Phe Arg Leu Ser Ala Lys Thr Arg Gln Gly Trp Gly Glu Pro  
 385 390 395 400  
 Leu Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro  
 405 410 415

Pro Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser Leu  
 420 425 430  
 Arg Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr  
 435 440 445  
 Phe Thr Met Gln Val Arg Glu Leu Pro Arg Gly Glu Trp Gln Thr Tyr  
 450 455 460  
 Ser Ser Ser Ile Ser His Glu Ala Thr Ala Cys Val Val Asp Arg Leu  
 465 470 475 480  
 Arg Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile  
 485 490 495  
 Gly Asp Ser Asp Phe Ser Ser Glu Thr Glu Ala Val Thr Thr Leu Gln  
 500 505 510  
 Asp Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr  
 515 520 525  
 Thr Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu  
 530 535 540  
 Asn Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Tyr  
 545 550 555 560  
 Glu Ala Gly Ser Gly Thr Glu Ala Lys Thr Leu Lys Asn Pro Ile Ala  
 565 570 575  
 Leu His Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser  
 580 585 590  
 Ser Ser Thr Ser Thr Met Cys Glu Leu Thr His Leu Lys Lys Tyr Arg  
 595 600 605  
 Arg Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro  
 610 615 620  
 Ala Ser Ala Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met  
 625 630 635 640  
 Ala Pro Gln Asn Val Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu  
 645 650 655  
 Val Thr Trp Asp Pro Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln  
 660 665 670  
 Gly Tyr Lys Ile Tyr Tyr Trp Glu Ala Asp Ser Gln Asn Glu Thr Glu  
 675 680 685  
 Lys Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Arg Leu Lys Asn  
 690 695 700  
 Leu Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala  
 705 710 715 720  
 Ala Gly Asp Gly Pro Lys Ser Asp Pro Gln Gln Gly Arg Thr His Gln  
 725 730 735  
 Ala Ala Pro Gly Ala Pro Ser Phe Leu Ala Phe Ser Glu Ile Thr Ser  
 740 745 750  
 Thr Thr Leu Asn Val Ser Trp Gly Glu Pro Ala Ala Ala Asn Gly Ile  
 755 760 765  
 Leu Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly  
 770 775 780  
 Val Ser Lys Val Val Thr Val Glu Val Arg Gly Asn Trp Gln Arg Trp  
 785 790 795 800  
 Leu Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val  
 805 810 815  
 Gln Ala Arg Thr Ile Thr Tyr Gly Pro Glu Leu Gln Ala Asn Ile Thr  
 820 825 830  
 Ala Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asp Val Leu Val  
 835 840 845  
 Thr Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly His Ser  
 850 855 860  
 Gly Asp Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp  
 865 870 875 880  
 Glu Gly Leu Trp Asp Met Phe Val Lys Asp Ile Pro Arg Ser Ala Thr

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<210> 36
<211> 540
<212> PRT
<213> Homo sapiens
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<400> 36															
Asx	Met	Thr	Ala	Tyr	Asn	Ile	Ile	Gly	Glu	Ser	Pro	Ala	Ser	Ala	Pro
1				5					10					15	
Val	Glu	Val	Phe	Val	Gly	Glu	Ala	Ala	Pro	Ala	Met	Ala	Pro	Gln	Asn
			20					25					30		
Val	Gln	Val	Thr	Pro	Leu	Thr	Ala	Ser	Gln	Leu	Glu	Val	Thr	Trp	Asp
		35					40					45			
Pro	Pro	Pro	Pro	Glu	Ser	Gln	Asn	Gly	Asn	Ile	Gln	Gly	Tyr	Lys	Ile
	50					55					60				
Tyr	Tyr	Trp	Glu	Ala	Asp	Ser	Gln	Asn	Glu	Thr	Glu	Lys	Met	Lys	Val
65				70					75					80	
Leu	Phe	Leu	Pro	Glu	Pro	Val	Val	Arg	Leu	Lys	Asn	Leu	Thr	Ser	His
				85					90					95	
Thr	Lys	Tyr	Leu	Val	Ser	Ile	Ser	Ala	Phe	Asn	Ala	Ala	Gly	Asp	Gly
			100					105					110		
Pro	Lys	Ser	Asp	Pro	Gln	Gln	Gly	Arg	Thr	His	Gln	Ala	Ala	Pro	Gly
		115					120					125			
Ala	Pro	Ser	Phe	Leu	Ala	Phe	Ser	Glu	Ile	Thr	Ser	Thr	Thr	Leu	Asn
	130					135					140				
Val	Ser	Trp	Gly	Glu	Pro	Ala	Ala	Ala	Asn	Gly	Ile	Leu	Gln	Gly	Tyr

145					150					155				160
Arg	Val	Val	Tyr	Glu	Pro	Leu	Ala	Pro	Val	Gln	Gly	Val	Ser	Lys
				165						170				175
Val	Thr	Val	Glu	Val	Arg	Gly	Asn	Trp	Gln	Arg	Trp	Leu	Lys	Val
			180					185					190	
Asp	Leu	Thr	Lys	Gly	Val	Thr	Tyr	Phe	Phe	Arg	Val	Gln	Ala	Arg
			195				200					205		
Ile	Thr	Tyr	Gly	Pro	Glu	Leu	Gln	Ala	Asn	Ile	Thr	Ala	Gly	Pro
	210					215				220				
Glu	Gly	Ser	Pro	Gly	Ser	Pro	Arg	Asp	Val	Leu	Val	Thr	Lys	Ser
225					230				235					240
Ser	Glu	Leu	Thr	Leu	Gln	Trp	Thr	Glu	Gly	His	Ser	Gly	Asp	Thr
				245					250					255
Thr	Thr	Gly	Tyr	Val	Ile	Glu	Ala	Arg	Pro	Ser	Asp	Glu	Gly	Leu
		260					265					270		
Asp	Met	Phe	Val	Lys	Asp	Ile	Pro	Arg	Ser	Ala	Thr	Ser	Tyr	Thr
	275					280					285			
Ser	Leu	Asp	Lys	Leu	Arg	Gln	Gly	Val	Thr	Tyr	Glu	Phe	Arg	Val
	290				295						300			
Ala	Val	Asn	Glu	Ala	Gly	Tyr	Gly	Glu	Pro	Ser	Asn	Pro	Ser	Thr
305					310				315					320
Val	Ser	Ala	Gln	Val	Glu	Ala	Pro	Phe	Tyr	Glu	Glu	Trp	Trp	Phe
			325					330						335
Leu	Val	Met	Ala	Leu	Ser	Ser	Leu	Ile	Val	Ile	Leu	Leu	Val	Val
	340						345						350	
Ala	Leu	Val	Leu	His	Gly	Gln	Asn	Lys	Lys	Tyr	Lys	Asn	Cys	Ser
	355					360					365			
Gly	Ala	Gly	Lys	Gly	Ile	Ser	Thr	Met	Glu	Glu	Ser	Val	Thr	Leu
	370				375						380			
Asn	Gly	Gly	Phe	Ala	Ala	Leu	Glu	Leu	Ser	Ser	Arg	His	Leu	Asn
385				390					395					400
Lys	Ser	Thr	Phe	Ser	Lys	Lys	Asn	Gly	Thr	Arg	Ser	Pro	Pro	Arg
			405					410						415
Ser	Pro	Gly	Gly	Leu	His	Tyr	Ser	Asp	Glu	Asp	Ile	Cys	Asn	Lys
		420					425					430		
Asn	Gly	Ala	Val	Leu	Thr	Glu	Ser	Val	Ser	Leu	Lys	Glu	Lys	Ser
	435					440						445		
Asp	Ala	Ser	Glu	Ser	Glu	Ala	Thr	Asp	Ser	Asp	Tyr	Glu	Asp	Ala
	450				455					460				Leu
Pro	Lys	His	Ser	Phe	Val	Asn	His	Tyr	Met	Ser	Asp	Pro	Thr	Tyr
465					470				475					480
Asn	Ser	Trp	Lys	Arg	Arg	Ala	Gln	Gly	Arg	Ala	Pro	Ala	Pro	His
			485					490						495
Tyr	Glu	Ala	Val	Ala	Gly	Ser	Glu	Ala	Gly	Ala	Gln	Leu	His	Pro
		500					505					510		
Ile	Thr	Thr	Gln	Ser	Ala	Gly	Gly	Val	Tyr	Thr	Pro	Ala	Gly	Pro
	515					520					525			
Ala	Arg	Thr	Pro	Leu	Thr	Gly	Phe	Ser	Ser	Phe	Val			
	530					535					540			

&lt;210&gt; 37

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

Met	Leu	Trp	Arg	Gln	Leu	Ile	Tyr	Trp	Gln	Leu	Leu	Ala	Leu	Phe	Phe
1				5					10					15	
Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Val	Ser	Gly	Arg

				20										25										30			
Thr	Asn	Lys	Val	Val	Ala	Arg	Ile	Val	Gln	Ser	His	Gln	Gln	Thr	Gly												
		35					40					45															
Arg	Ser	Gly	Ser	Arg	Arg	Glu	Lys	Val	Arg	Glu	Arg	Ser	His	Pro	Lys												
	50					55					60																
Thr	Gly	Thr	Val	Asp	Asn	Asn	Thr	Ser	Thr	Asp	Leu	Lys	Ser	Leu	Arg												
65					70					75																	80
Pro	Asp	Glu	Leu	Pro	His	Pro	Glu	Val	Asp	Asp	Leu	Ala	Gln	Ile	Thr												
				85					90					95													
Thr	Phe	Trp	Gly	Gln	Ser	Pro	Gln	Thr	Gly	Gly	Leu	Pro	Pro	Asp	Cys												
			100					105					110														
Ser	Lys	Cys	Cys	His	Gly	Asp	Tyr	Ser	Phe	Arg	Gly	Tyr	Gln	Gly	Pro												
		115					120					125															
Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile	Pro	Gly	Asn	His	Gly	Asn	Asn												
	130					135				140																	
Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu	Gly	Ala	Lys	Gly	Glu	Lys	Gly												
145					150					155																	160
Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Gln	His	Gly	Pro												
			165					170						175													
Lys	Gly	Glu	Lys	Gly	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Leu	Gln	Ile	Ala												
			180					185					190														
Phe	Met	Ala	Ser	Leu	Ala	Thr	His	Phe	Ser	Asn	Gln	Asn	Ser	Gly	Ile												
		195					200				205																
Ile	Phe	Ser	Ser	Val	Glu	Thr	Asn	Ile	Gly	Asn	Phe	Phe	Asp	Val	Met												
	210					215				220																	
Thr	Gly	Arg	Phe	Gly	Ala	Pro	Val	Ser	Gly	Val	Tyr	Phe	Phe	Thr	Phe												
225					230					235																	240
Ser	Met	Met	Lys	His	Glu	Asp	Val	Glu	Glu	Val	Tyr	Val	Tyr	Leu	Met												
				245				250					255														
His	Asn	Gly	Asn	Thr	Val	Phe	Ser	Met	Tyr	Ser	Tyr	Glu	Met	Lys</													

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<210> 38
<211> 246
<212> PRT
<213> Homo sapiens
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<400> 38															
Met	Leu	Trp	Arg	Gln	Leu	Ile	Tyr	Trp	Gln	Leu	Leu	Ala	Leu	Phe	Phe
1				5					10					15	
Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Ser	Pro	Gln	Thr
			20					25					30		
Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly	Asp	Tyr	Ser
		35					40					45			
Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile
	50					55					60				
Pro	Gly	Asn	His	Gly	Asn	Asn	Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu
65				70						75					80
Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly
				85					90					95	
Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly	Glu	Lys	Gly	Tyr	Pro	Gly	Ile
			100					105					110		
Pro	Pro	Glu	Leu	Gln	Ile	Ala	Phe	Met	Ala	Ser	Leu	Ala	Thr	His	Phe

[illegible]

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<210> 39
<211> 675
<212> PRT
<213> Homo sapiens
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<400> 39															
Met 1	Thr	Thr	Ser 5	His	Met	Asn	Gly	His	Val 10	Thr	Glu	Glu	Ser 15	Asp	Ser
Glu	Val	Lys	Asn 20	Val	Asp	Leu	Ala	Ser 25	Pro	Glu	Glu	His	Gln 30	Lys	His
Arg	Glu	Met 35	Ala	Val	Asp	Cys	Pro 40	Gly	Asp	Leu	Gly	Thr 45	Arg	Met	Met
Pro	Ile 50	Arg	Arg	Ser	Ala	Gln 55	Leu	Glu	Arg	Ile	Arg 60	Gln	Gln	Gln	Glu
Asp 65	Met	Arg	Arg	Arg	Arg 70	Glu	Glu	Glu	Gly	Lys 75	Lys	Gln	Glu	Leu	Asp 80
Leu	Asn	Ser	Ser	Met 85	Arg	Leu	Lys	Lys	Leu 90	Ala	Gln	Ile	Pro 95	Pro	Lys
Thr	Gly	Ile	Asp 100	Asn	Pro	Met	Phe	Asp 105	Thr	Glu	Glu	Gly	Ile 110	Val	Leu
Glu	Ser	Pro	His 115	Tyr	Ala	Val	Lys 120	Ile	Leu	Glu	Ile	Glu	Asp 125	Leu	Phe
Ser	Ser	Leu	Lys 130	His	Ile	Gln 135	His	Thr	Leu	Val	Asp 140	Ser	Gln	Ser	Gln
Glu 145	Asp	Ile	Ser	Leu 150	Leu	Gln	Leu	Val	Gln 155	Asn	Lys	Asp	Phe	Gln	160
Asn	Ala	Phe	Lys 165	Ile	His	Asn	Ala	Ile	Thr 170	Val	His	Met	Asn 175	Lys	Ala
Ser	Pro	Pro	Phe 180	Pro	Leu	Ile	Ser	Asn 185	Ala	Gln	Asp	Leu	Ala 190	Gln	Glu
Val	Gln	Thr	Val 195	Leu	Lys	Pro	Val	His 200	His	Lys	Glu	Gly	Gln 205	Glu	Leu
Thr	Ala	Leu	Leu 210	Asn	Thr	Pro 215	His	Ile	Gln	Ala	Leu	Leu	Leu 220	Ala	His
Asp 225	Lys	Val	Ala	Glu	Gln	Glu	Met	Gln	Leu	Glu	Pro	Ile	Thr 240	Asp	Glu
Arg	Val	Tyr	Glu 245	Ser	Ile	Gly	Gln	Tyr	Gly	Gly	Glu	Thr	Val 255	Lys	Ile
Val	Arg	Ile	Glu 260	Lys	Ala	Arg	Asp	Ile	Pro	Leu	Gly	Ala	Thr 270	Val	Arg
Asn	Glu	Met	Asp	Ser	Val	Ile	Ile	Ser	Arg	Ile	Val	Lys	Gly	Gly	Ala



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      275      280      285
Ala Glu Lys Ser Gly Leu Leu His Glu Gly Asp Glu Val Leu Glu Ile
  290      295      300
Asn Gly Ile Glu Ile Arg Gly Lys Asp Val Asn Glu Val Phe Asp Leu
  305      310      315      320
Leu Ser Asp Met His Gly Thr Leu Thr Phe Val Leu Ile Pro Ser Gln
      325      330      335
Gln Ile Lys Pro Pro Pro Ala Lys Glu Thr Val Ile His Val Lys Ala
      340      345      350
His Phe Asp Tyr Asp Pro Ser Asp Asp Pro Tyr Val Pro Cys Arg Glu
      355      360      365
Leu Gly Leu Ser Phe Gln Lys Gly Asp Ile Leu His Val Ile Ser Gln
      370      375      380
Glu Asp Pro Asn Trp Trp Gln Ala Tyr Arg Glu Gly Asp Glu Asp Asn
  385      390      395      400
Gln Pro Leu Ala Gly Leu Val Pro Gly Lys Ser Phe Gln Gln Gln Arg
      405      410      415
Glu Ala Met Lys Gln Thr Ile Glu Glu Asp Lys Glu Pro Glu Lys Ser
      420      425      430
Gly Lys Leu Trp Cys Ala Lys Lys Asn Lys Lys Lys Arg Lys Lys Val
      435      440      445
Leu Tyr Asn Ala Asn Lys Asn Asp Asp Tyr Asp Asn Glu Glu Ile Leu
      450      455      460
Thr Tyr Glu Glu Met Ser Leu Tyr His Gln Pro Ala Asn Arg Lys Arg
  465      470      475      480
Pro Ile Ile Leu Ile Gly Pro Gln Asn Cys Gly Gln Asn Glu Leu Arg
      485      490      495
Gln Arg Leu Met Asn Lys Glu Lys Asp Arg Phe Ala Ser Ala Val Pro
      500      505      510
His Thr Thr Arg Ser Arg Arg Asp Gln Glu Val Ala Gly Arg Asp Tyr
      515      520      525
His Phe Val Ser Arg Gln Ala Phe Glu Ala Asp Ile Ala Ala Gly Lys
      530      535      540
Phe Ile Glu His Gly Glu Phe Glu Lys Asn Leu Tyr Gly Thr Ser Ile
  545      550      555      560
Asp Ser Val Arg Gln Val Ile Asn Ser Gly Lys Ile Cys Leu Leu Ser
      565      570      575
Leu Arg Thr Gln Ser Leu Lys Thr Leu Arg Asn Ser Asp Leu Lys Pro
      580      585      590
Tyr Ile Ile Phe Ile Ala Pro Pro Ser Gln Glu Arg Leu Arg Ala Leu
      595      600      605
Leu Ala Lys Glu Gly Lys Asn Pro Lys Pro Glu Glu Leu Arg Glu Ile
      610      615      620
Ile Glu Lys Thr Arg Glu Met Glu Gln Asn Asn Gly His Tyr Phe Asp
  625      630      635      640
Thr Ala Ile Val Asn Ser Asp Leu Asp Lys Ala Tyr Gln Glu Leu Leu
      645      650      655
Arg Leu Ile Asn Lys Leu Asp Thr Glu Pro Gln Trp Val Pro Ser Thr
      660      665      670
Trp Leu Arg
      675

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&lt;210&gt; 40

&lt;211&gt; 675

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

Met Thr Thr Ser His Met Asn Gly His Val Thr Glu Glu Ser Asp Ser

1	5	10	15
Glu Val Lys Asn Val Asp Leu Ala Ser Pro Glu Glu His Gln Lys His			
20	25	30	
Arg Glu Met Ala Val Asp Cys Pro Gly Asp Leu Gly Thr Arg Met Met			
35	40	45	
Pro Ile Arg Arg Ser Ala Gln Leu Glu Arg Ile Arg Gln Gln Gln Glu			
50	55	60	
Asp Met Arg Arg Arg Arg Glu Glu Glu Gly Lys Lys Gln Glu Leu Asp			
65	70	75	80
Leu Asn Ser Ser Met Arg Leu Lys Lys Leu Ala Gln Ile Pro Pro Lys			
85	90	95	
Thr Gly Ile Asp Asn Pro Met Phe Asp Thr Glu Glu Gly Ile Val Leu			
100	105	110	
Glu Ser Pro His Tyr Ala Val Lys Ile Leu Glu Ile Glu Asp Leu Phe			
115	120	125	
Ser Ser Leu Lys His Ile Gln His Thr Leu Val Asp Ser Gln Ser Gln			
130	135	140	
Glu Asp Ile Ser Leu Leu Leu Gln Leu Val Gln Asn Lys Asp Phe Gln			
145	150	155	160
Asn Ala Phe Lys Ile His Asn Ala Ile Thr Val His Met Asn Lys Ala			
165	170	175	
Ser Pro Pro Phe Pro Leu Ile Ser Asn Ala Gln Asp Leu Ala Gln Glu			
180	185	190	
Val Gln Thr Val Leu Lys Pro Val His His Lys Glu Gly Gln Glu Leu			
195	200	205	
Thr Ala Leu Leu Asn Thr Pro His Ile Gln Ala Leu Leu Leu Ala His			
210	215	220	
Asp Lys Val Ala Glu Gln Glu Met Gln Leu Glu Pro Ile Thr Asp Glu			
225	230	235	240
Arg Val Tyr Glu Ser Ile Gly Gln Tyr Gly Gly Glu Thr Val Lys Ile			
245	250	255	
Val Arg Ile Glu Lys Ala Arg Asp Ile Pro Leu Gly Ala Thr Val Arg			
260	265	270	
Asn Glu Met Asp Ser Val Ile Ile Ser Arg Ile Val Lys Gly Gly Ala			
275	280	285	
Ala Glu Lys Ser Gly Leu Leu His Glu Gly Asp Glu Val Leu Glu Ile			
290	295	300	
Asn Gly Ile Glu Ile Arg Gly Lys Asp Val Asn Glu Val Phe Asp Leu			
305	310	315	320
Leu Ser Asp Met His Gly Thr Leu Thr Phe Val Leu Ile Pro Ser Gln			
325	330	335	
Gln Ile Lys Pro Pro Pro Ala Lys Glu Thr Val Ile His Val Lys Ala			
340	345	350	
His Phe Asp Tyr Asp Pro Ser Asp Asp Pro Tyr Val Pro Cys Arg Glu			
355	360	365	
Leu Gly Leu Ser Phe Gln Lys Gly Asp Ile Leu His Val Ile Ser Gln			
370	375	380	
Glu Asp Pro Asn Trp Trp Gln Ala Tyr Arg Glu Gly Asp Glu Asp Asn			
385	390	395	400
Gln Pro Leu Ala Gly Leu Val Pro Gly Lys Ser Phe Gln Gln Gln Arg			
405	410	415	
Glu Ala Met Lys Gln Thr Ile Glu Glu Asp Lys Glu Pro Glu Lys Ser			
420	425	430	
Gly Lys Leu Trp Cys Ala Lys Lys Asn Lys Lys Lys Arg Lys Lys Val			
435	440	445	
Leu Tyr Asn Ala Asn Lys Asn Asp Asp Tyr Asp Asn Glu Glu Ile Leu			
450	455	460	
Thr Tyr Glu Glu Met Ser Leu Tyr His Gln Pro Ala Asn Arg Lys Arg			
465	470	475	480

Pro Ile Ile Leu Ile Gly Pro Gln Asn Cys Gly Gln Asn Glu Leu Arg  
 485 490 495  
 Gln Arg Leu Met Asn Lys Glu Lys Asp Arg Phe Ala Ser Ala Val Pro  
 500 505 510  
 His Thr Thr Arg Ser Arg Arg Asp Gln Glu Val Ala Gly Arg Asp Tyr  
 515 520 525  
 His Phe Val Ser Arg Gln Ala Phe Glu Ala Asp Ile Ala Ala Gly Lys  
 530 535 540  
 Phe Ile Glu His Gly Glu Phe Glu Lys Asn Leu Tyr Gly Thr Ser Ile  
 545 550 555 560  
 Asp Ser Val Arg Gln Val Ile Asn Ser Gly Lys Ile Cys Leu Leu Ser  
 565 570 575  
 Leu Arg Thr Gln Ser Leu Lys Thr Leu Arg Asn Ser Asp Leu Lys Pro  
 580 585 590  
 Tyr Ile Ile Phe Ile Ala Pro Pro Ser Gln Glu Arg Leu Arg Ala Leu  
 595 600 605  
 Leu Ala Lys Glu Gly Lys Asn Pro Lys Pro Glu Glu Leu Arg Glu Ile  
 610 615 620  
 Ile Glu Lys Thr Arg Glu Met Glu Gln Asn Asn Gly His Tyr Phe Asp  
 625 630 635 640  
 Thr Ala Ile Val Asn Ser Asp Leu Asp Lys Ala Tyr Gln Glu Leu Leu  
 645 650 655  
 Arg Leu Ile Asn Lys Leu Asp Thr Glu Pro Gln Trp Val Pro Ser Thr  
 660 665 670  
 Trp Leu Arg  
 675

&lt;210&gt; 41

&lt;211&gt; 957

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

Met Ser Leu Val Ser Gln Asn Ser Arg Arg Arg Arg Arg Val Ala  
 1 5 10 15  
 Lys Ala Thr Ala His Asn Ser Ser Trp Gly Glu Met Gln Ala Pro Asn  
 20 25 30  
 Ala Pro Gly Leu Pro Ala Asp Val Pro Gly Ser Asp Val Pro Gln Gly  
 35 40 45  
 Pro Ser Asp Ser Gln Ile Leu Gln Gly Leu Cys Ala Ser Glu Gly Pro  
 50 55 60  
 Ser Thr Ser Val Leu Pro Thr Ser Ala Glu Gly Pro Ser Thr Phe Val  
 65 70 75 80  
 Pro Pro Thr Ile Ser Glu Ala Ser Ser Ala Ser Gly Gln Pro Thr Ile  
 85 90 95  
 Ser Glu Gly Pro Gly Thr Ser Val Leu Pro Thr Pro Ser Glu Gly Leu  
 100 105 110  
 Ser Thr Ser Gly Pro Pro Thr Ile Ser Lys Gly Leu Cys Thr Ser Val  
 115 120 125  
 Thr Leu Ala Ala Ser Glu Gly Arg Asn Thr Ser Arg Pro Pro Thr Ser  
 130 135 140  
 Ser Glu Glu Pro Ser Thr Val Pro Pro Thr Ala Ser Glu Val Pro  
 145 150 155 160  
 Ser Thr Ser Leu Pro Pro Thr Pro Gly Glu Gly Thr Ser Thr Ser Val  
 165 170 175  
 Pro Pro Thr Ala Tyr Glu Gly Pro Ser Thr Ser Val Val Pro Thr Pro  
 180 185 190  
 Asp Glu Gly Pro Ser Thr Ser Val Leu Pro Thr Pro Gly Glu Gly Pro  
 195 200 205

Gly	Thr	Ser	Val	Pro	Leu	Ala	Ala	Thr	Glu	Gly	Leu	Ser	Thr	Ser	Val
210						215					220				
Gln	Ala	Thr	Pro	Asp	Glu	Gly	Pro	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala
225					230					235					240
Thr	Glu	Gly	Leu	Ser	Thr	Pro	Val	Pro	Pro	Thr	Arg	Asp	Glu	Gly	Pro
				245					250					255	
Ser	Thr	Ser	Val	Pro	Ala	Thr	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Ser	Val
			260					265					270		
Leu	Pro	Ala	Ala	Ser	Asp	Gly	Gln	Ser	Ile	Ser	Leu	Val	Pro	Thr	Arg
		275					280					285			
Gly	Lys	Gly	Ser	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala	Thr	Glu	Gly	Leu
290						295					300				
Ser	Thr	Ser	Val	Gln	Pro	Thr	Ala	Gly	Glu	Gly	Ser	Ser	Thr	Ser	Val
305				310						315					320
Pro	Pro	Thr	Pro	Gly	Gly	Gly	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala
				325					330					335	
Thr	Glu	Glu	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Pro	Gly	Glu	Gly	Pro
			340					345					350		
Ser	Thr	Ser	Val	Leu	Pro	Ile	Pro	Gly	Glu	Gly	Leu	Ser	Thr	Ser	Val
			355				360					365			
Pro	Pro	Thr	Ala	Ser	Asp	Gly	Ser	Asp	Thr	Ser	Val	Pro	Pro	Thr	Pro
			370			375					380				
Gly	Glu	Gly	Ala	Ser	Thr	Leu	Val	Gln	Pro	Thr	Ala	Pro	Asp	Gly	Pro
385					390					395					400
Gly	Ser	Ser	Val	Leu	Pro	Asn	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Leu	Phe
				405					410					415	
Ser	Ser	Ser	Ala	Ser	Val	Asp	Arg	Asn	Pro	Ser	Lys	Cys	Ser	Leu	Val
			420				425					430			
Leu	Pro	Ser	Pro	Arg	Val	Thr	Lys	Ala	Ser	Val	Asp	Ser	Asp	Ser	Glu
			435				440					445			
Gly	Pro	Lys	Gly	Ala	Glu	Gly	Pro	Ile	Glu	Phe	Glu	Val	Leu	Arg	Asp
450						455					460				
Cys	Glu	Ser	Pro	Asn	Ser	Ile	Ser	Ile	Met	Gly	Leu	Asn	Thr	Ser	Arg
465					470					475					480
Val	Ala	Ile	Thr	Leu	Lys	Pro	Gln	Asp	Pro	Met	Glu	Gln	Asn	Val	Ala
				485					490					495	
Glu	Leu	Leu	Gln	Phe	Leu	Leu	Val	Lys	Asp	Gln	Ser	Lys	Tyr	Pro	Ile
			500					505					510		
Arg	Glu	Ser	Glu	Met	Arg	Glu	Tyr	Ile	Val	Lys	Glu	Tyr	Arg	Asn	Gln
			515				520					525			
Phe	Pro	Glu	Ile	Leu	Arg	Arg	Ala	Ala	Ala	His	Leu	Glu	Cys	Ile	Phe
			530			535					540				
Arg	Phe	Glu	Leu	Arg	Glu	Leu	Asp	Pro	Glu	Ala	His	Thr	Tyr	Ile	Leu
545					550					555					560
Leu	Asn	Lys	Leu	Gly	Pro	Val	Pro	Phe	Glu	Gly	Leu	Glu	Glu	Ser	Pro
				565					570					575	
Asn	Gly	Pro	Lys	Met	Gly	Leu	Leu	Met	Met	Ile	Leu	Gly	Gln	Ile	Phe
			580					585					590		
Leu	Asn	Gly	Asn	Gln	Ala	Lys	Glu	Ala	Glu	Ile	Trp	Glu	Met	Leu	Trp
		595					600					605			
Arg	Met	Gly	Val	Gln	Arg	Glu	Arg	Arg	Leu	Ser	Ile	Phe	Gly	Asn	Pro
						615					620				
Lys	Arg	Leu	Leu	Ser	Val	Glu	Phe	Val	Trp	Gln	Arg	Tyr	Leu	Asp	Tyr
625					630					635					640
Arg	Pro	Val	Thr	Asp	Cys	Lys	Pro	Val	Glu	Tyr	Glu	Phe	Phe	Trp	Gly
				645					650					655	
Pro	Arg	Ser	His	Leu	Glu	Thr	Thr	Lys	Met	Lys	Ile	Leu	Lys	Phe	Met
			660					665					670		
Ala	Lys	Ile	Tyr	Asn	Lys	Asp	Pro	Met	Asp	Trp	Pro	Glu	Lys	Tyr	Asn

675	680	685
Glu Ala Leu Glu Glu Asp	Ala Ala Arg Ala Phe Ala	Glu Gly Trp Gln
690	695	700
Ala Leu Pro His Phe Arg Arg	Pro Phe Phe Glu Glu Ala Ala	Ala Glu
705	710	715
Val Pro Ser Pro Asp Ser Glu	Val Ser Ser Tyr Ser Ser Lys Tyr	Ala
725	730	735
Pro His Ser Trp Pro Glu Ser	Arg Leu Glu Ser Lys Ala Arg Lys	Leu
740	745	750
Val Gln Leu Phe Leu Leu Met	Asp Ser Thr Lys Leu Pro Ile Pro	Lys
755	760	765
Lys Gly Ile Leu Tyr Tyr Ile	Gly Arg Glu Cys Ser Lys Val Phe	Pro
770	775	780
Asp Leu Leu Asn Arg Ala Ala	Arg Thr Leu Asn His Val Tyr Gly Thr	
785	790	795
Glu Leu Val Val Leu Asp Pro	Arg Asn His Ser Tyr Thr Leu Tyr Asn	
805	810	815
Arg Arg Glu Met Glu Glu Thr	Glu Glu Ile Val Asp Ser Pro Asn Arg	
820	825	830
Pro Gly Asn Asn Phe Leu Met	Gln Val Leu Ser Phe Ile Phe Ile Met	
835	840	845
Gly Asn His Ala Arg Glu Ser	Ala Val Trp Ala Phe Leu Arg Gly Leu	
850	855	860
Gly Val Gln Ala Gly Arg Lys	His Val Ile Thr Cys Arg Tyr Leu Ser	
865	870	875
Gln Arg Tyr Ile Asp Ser Leu	Arg Val Pro Asp Ser Asp Pro Val Gln	
885	890	895
Tyr Glu Phe Val Trp Gly Pro	Arg Ala Arg Leu Glu Thr Ser Lys Met	
900	905	910
Lys Ala Leu Arg Tyr Val Ala	Arg Ile His Arg Lys Glu Pro Gln Asp	
915	920	925
Trp Pro Gln Gln Tyr Arg Glu	Ala Met Glu Asp Glu Ala Asn Arg Ala	
930	935	940
Asp Val Gly His Arg Gln Ile	Phe Val His Asn Phe Arg	
945	950	955

&lt;210&gt; 42

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser	
1	5
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn	
20	25
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro	
35	40
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly	
50	55
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys	
65	70
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly	
85	90
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys	
100	105
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr	
115	120
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys	
125	

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      130              135              140
Gly His Phe Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser
145              150              155              160
Asp Thr Ser Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp
      165              170              175
Arg Gln Thr Cys Phe Gly Lys Lys Leu Ile Lys Asp Glu Asn Glu Cys
      180              185              190
Glu Gln Asn Asn Gly Gly Cys Ser Glu Ile Cys Val Asn Leu Lys Asn
      195              200              205
Ser Tyr Arg Cys Glu Cys Gly Val Gly Arg Val Leu Arg Ser Asp Gly
      210              215              220
Lys Thr Cys Glu Gly Glu Asn Gly Gln Lys Gly Thr Gln Ile Lys Ser
      225              230              235              240
Pro Glu Glu Ala Thr Gly Leu Phe Ser Asp Val Gln Glu Thr Ala Leu
      245              250              255
Val Ser Glu Glu Ser Asn Arg Leu Ala Val Gln Arg Asn Asp Lys Arg
      260              265              270
Arg Ser Ser Thr Leu Arg Ile Leu Thr Leu Trp Thr Glu Phe Ser Phe
      275              280              285
Asp Phe Val Ser Lys Ile
      290

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<210> 43
<211> 468
<212> PRT
<213> Homo sapiens

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```

      <400> 43
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
1      5      10      15
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
      20      25      30
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
      35      40      45
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
      50      55      60
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
      65      70      75      80
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
      85      90      95
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
      100      105      110
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
      115      120      125
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
      130      135      140
Gly His Val Glu Gly Cys His Asn Asn Asn Gly Gly Cys Ser His Ser
      145      150      155      160
Cys Leu Gly Ser Glu Lys Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu
      165      170      175
Val Leu Ser Glu Asp Asn His Thr Cys Gln Val Pro Val Leu Cys Lys
      180      185      190
Ser Asn Ala Ile Glu Val Asn Ile Pro Arg Glu Leu Val Gly Gly Leu
      195      200      205
Glu Leu Phe Leu Thr Asn Thr Ser Cys Arg Gly Val Ser Asn Gly Thr
      210      215      220
His Val Asn Ile Leu Phe Ser Leu Lys Thr Cys Gly Thr Val Val Asp
      225      230      235      240
Val Val Asn Asp Lys Ile Val Ala Ser Asn Leu Val Thr Gly Leu Pro

```

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      245      250      255
Lys Gln Thr Pro Gly Ser Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys
      260      265      270
Leu Leu Ile Pro Val Thr Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser
      275      280      285
Glu Gly Tyr Val Pro Asn Leu Arg Asn Ser Pro Leu Glu Ile Met Ser
      290      295      300
Arg Asn His Gly Ile Phe Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn
      305      310      315      320
Glu Phe Glu Glu Pro Tyr Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg
      325      330      335
Asp Ser Leu Tyr Phe Gly Ile Glu Pro Val Val His Val Ser Gly Leu
      340      345      350
Glu Ser Leu Val Glu Ser Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp
      355      360      365
Glu Val Leu Lys Tyr Tyr Leu Ile Arg Asp Gly Cys Val Ser Asp Asp
      370      375      380
Ser Val Lys Gln Tyr Thr Ser Arg Asp His Leu Ala Lys His Phe Gln
      385      390      395      400
Val Pro Val Phe Lys Phe Val Gly Lys Asp His Lys Glu Val Phe Leu
      405      410      415
His Cys Arg Val Leu Val Cys Gly Val Leu Asp Glu Arg Ser Arg Cys
      420      425      430
Ala Gln Gly Cys His Arg Arg Met Arg Arg Gly Ala Gly Gly Glu Asp
      435      440      445
Ser Ala Gly Leu Gln Gly Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile
      450      455      460
Asp Trp Glu Asp
465

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<210> 44
<211> 238
<212> PRT
<213> Homo sapiens

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```

      <400> 44
Met Val Leu Leu Leu Leu Val Ala Ile Pro Leu Leu Val His Ser Ser
  1      5      10      15
Arg Gly Pro Ala His Tyr Glu Met Leu Gly Arg Cys Arg Met Val Cys
      20      25      30
Asp Pro His Gly Pro Arg Gly Pro Gly Pro Asp Gly Ala Pro Ala Ser
      35      40      45
Val Pro Pro Phe Pro Pro Gly Ala Lys Gly Glu Val Gly Arg Arg Gly
      50      55      60
Lys Ala Gly Leu Arg Gly Pro Pro Gly Pro Pro Gly Pro Arg Gly Pro
      65      70      75      80
Pro Gly Glu Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly
      85      90      95
Pro Gly Gly Val Ala Pro Ala Ala Gly Tyr Val Pro Arg Ile Ala Phe
      100      105      110
Tyr Ala Gly Leu Arg Arg Pro His Glu Gly Tyr Glu Val Leu Arg Phe
      115      120      125
Asp Asp Val Val Thr Asn Val Gly Asn Ala Tyr Glu Ala Ala Ser Gly
      130      135      140
Lys Phe Thr Cys Pro Met Pro Gly Val Tyr Phe Phe Ala Tyr His Val
      145      150      155      160
Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Met Lys
      165      170      175
Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln Asn

```

180 185 190  
 Tyr Asp Tyr Ala Ser Asn Ser Val Ile Leu His Leu Asp Val Gly Asp  
 195 200 205  
 Glu Val Phe Ile Lys Leu Asp Gly Gly Lys Val His Gly Gly Asn Thr  
 210 215 220  
 Asn Lys Tyr Ser Thr Phe Ser Gly Phe Ile Ile Tyr Pro Asp  
 225 230 235

<210> 45  
 <211> 267  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Val Leu Leu Leu Leu Val Ala Ile Pro Leu Leu Val His Ser Ser  
 1 5 10 15  
 Arg Gly Pro Ala His Tyr Glu Met Leu Gly Arg Cys Arg Met Val Cys  
 20 25 30  
 Asp Pro His Gly Pro Arg Gly Pro Gly Pro Asp Gly Ala Pro Ala Ser  
 35 40 45  
 Val Pro Pro Phe Pro Pro Gly Ala Lys Gly Glu Val Gly Arg Arg Gly  
 50 55 60  
 Lys Ala Gly Leu Arg Gly Pro Pro Gly Pro Pro Gly Pro Arg Gly Pro  
 65 70 75 80  
 Pro Gly Glu Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly  
 85 90 95  
 Leu Arg Gly Pro Pro Gly Pro Pro Gly Pro Arg Gly Pro Pro Gly Glu  
 100 105 110  
 Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly Pro Gly Gly  
 115 120 125  
 Val Ala Pro Ala Ala Gly Tyr Val Pro Arg Ile Ala Phe Tyr Ala Gly  
 130 135 140  
 Leu Arg Arg Pro His Glu Gly Tyr Glu Val Leu Arg Phe Asp Asp Val  
 145 150 155 160  
 Val Thr Asn Val Gly Asn Ala Tyr Glu Ala Ala Ser Gly Lys Phe Thr  
 165 170 175  
 Cys Pro Met Pro Gly Val Tyr Phe Phe Ala Tyr His Val Leu Met Arg  
 180 185 190  
 Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Met Lys Asn Gly Gln  
 195 200 205  
 Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln Asn Tyr Asp Tyr  
 210 215 220  
 Ala Ser Asn Ser Val Ile Leu His Leu Asp Val Gly Asp Glu Val Phe  
 225 230 235 240  
 Ile Lys Leu Asp Gly Gly Lys Val His Gly Gly Asn Thr Asn Lys Tyr  
 245 250 255  
 Ser Thr Phe Ser Gly Phe Ile Ile Tyr Pro Asp  
 260 265

<210> 46  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Gly Gln Leu Cys Trp Leu Pro Leu Leu Ala Pro Leu Leu Leu Leu  
 1 5 10 15  
 Arg Pro Pro Gly Val Gln Ser Ala Gly Pro Ile Arg Ala Phe Val Val  
 20 25 30



Pro His Ser His Met Asp Val Gly Trp Val Tyr Thr Val Gln Glu Ser  
 35 40 45  
 Met Arg Ala Tyr Ala Ala Asn Val Tyr Thr Ser Val Val Glu Glu Leu  
 50 55 60  
 Ala Arg Gly Gln Gln Arg Arg Phe Ile Ala Val Glu Gln Glu Phe Phe  
 65 70 75 80  
 Arg Leu Trp Trp Asp Gly Val Ala Ser Asp Gln Gln Lys Tyr Gln Val  
 85 90 95  
 Arg Gln Leu Leu Glu Glu Gly Arg Leu Glu Phe Val Ile Gly Gly Gln  
 100 105 110  
 Val Met His Asp Glu Ala Val Thr His Leu Asp Asp Gln Ile Leu Gln  
 115 120 125  
 Leu Thr Gly Leu Ala Thr Leu Pro Cys Thr Gln Gly Pro Ser Gly Pro  
 130 135 140  
 Pro Val Gly Leu Gly His Gly Ile Arg Thr Pro Arg Phe  
 145 150 155

<210> 47  
 <211> 1009  
 <212> PRT  
 <213> Homo sapiens

<400> 47  
 Met Gly Gln Leu Cys Trp Leu Pro Leu Leu Ala Pro Leu Leu Leu Leu  
 1 5 10 15  
 Arg Pro Pro Gly Val Gln Ser Ala Gly Pro Ile Arg Ala Phe Val Val  
 20 25 30  
 Pro His Ser His Met Asp Val Gly Trp Val Tyr Thr Val Gln Glu Ser  
 35 40 45  
 Met Arg Ala Tyr Ala Ala Asn Val Tyr Thr Ser Val Val Glu Glu Leu  
 50 55 60  
 Ala Arg Gly Gln Gln Arg Arg Phe Ile Ala Val Glu Gln Glu Phe Phe  
 65 70 75 80  
 Arg Leu Trp Trp Asp Gly Val Ala Ser Asp Gln Gln Lys Tyr Gln Val  
 85 90 95  
 Arg Gln Leu Leu Glu Glu Gly Arg Leu Glu Phe Val Ile Gly Gly Gln  
 100 105 110  
 Val Met His Asp Glu Ala Val Thr His Leu Asp Asp Gln Ile Leu Gln  
 115 120 125  
 Leu Thr Gly Gly His Gly Phe Leu Tyr Glu Thr Phe Gly Ile Arg Pro  
 130 135 140  
 Gln Phe Ser Trp His Val Asp Pro Phe Gly Ala Ser Ala Thr Thr Pro  
 145 150 155 160  
 Thr Leu Phe Ala Leu Ala Gly Phe Asn Ala His Leu Gly Ser Arg Ile  
 165 170 175  
 Asp Tyr Asp Leu Lys Ala Ala Met Gln Glu Ala Arg Gly Leu Gln Phe  
 180 185 190  
 Val Trp Arg Gly Ser Pro Ser Leu Ser Glu Arg Gln Glu Ile Phe Thr  
 195 200 205  
 His Ile Met Asp Gln Tyr Ser Tyr Cys Thr Pro Ser His Ile Pro Phe  
 210 215 220  
 Ser Asn Arg Ser Gly Phe Tyr Trp Asn Gly Val Ala Val Phe Pro Lys  
 225 230 235 240  
 Pro Pro Gln Asp Gly Val Tyr Pro Asn Met Ser Glu Pro Val Thr Pro  
 245 250 255  
 Ala Asn Ile Asn Leu Tyr Ala Glu Ala Leu Val Ala Asn Val Lys Gln  
 260 265 270  
 Arg Ala Ala Trp Phe Arg Thr Pro His Val Leu Trp Pro Trp Gly Cys  
 275 280 285

Asp	Lys	Gln	Phe	Phe	Asn	Ala	Ser	Val	Gln	Phe	Ala	Asn	Met	Asp	Pro
290						295					300				
Leu	Leu	Asp	His	Ile	Asn	Ser	His	Ala	Ala	Glu	Leu	Gly	Val	Ser	Val
305					310					315					320
Gln	Tyr	Ala	Thr	Leu	Gly	Asp	Tyr	Phe	Arg	Ala	Leu	His	Ala	Leu	Asn
				325					330						335
Val	Thr	Trp	Arg	Val	Arg	Asp	His	His	Asp	Phe	Leu	Pro	Tyr	Ser	Thr
			340					345					350		
Glu	Pro	Phe	Gln	Ala	Trp	Thr	Gly	Phe	Tyr	Thr	Ser	Arg	Ser	Ser	Leu
		355					360					365			
Lys	Gly	Leu	Ala	Arg	Arg	Ala	Ser	Ala	Leu	Leu	Tyr	Ala	Gly	Glu	Ser
370						375					380				
Met	Phe	Thr	Arg	Tyr	Leu	Trp	Pro	Ala	Pro	Arg	Gly	His	Leu	Asp	Pro
385					390					395					400
Thr	Trp	Ala	Leu	Gln	Gln	Leu	Gln	Gln	Leu	Arg	Trp	Ala	Val	Ser	Glu
				405					410						415
Val	Gln	His	His	Asp	Ala	Ile	Thr	Gly	Thr	Glu	Ser	Pro	Lys	Val	Arg
			420					425					430		
Asp	Met	Tyr	Ala	Thr	His	Leu	Ala	Ser	Gly	Met	Leu	Gly	Met	Arg	Lys
		435					440					445			
Leu	Met	Ala	Ser	Ile	Val	Leu	Asp	Glu	Leu	Gln	Pro	Gln	Ala	Pro	Met
450						455					460				
Ala	Ala	Ser	Ser	Asp	Ala	Gly	Pro	Ala	Gly	His	Phe	Ala	Ser	Val	Tyr
465					470					475					480
Asn	Pro	Leu	Ala	Trp	Thr	Val	Thr	Thr	Ile	Val	Thr	Leu	Thr	Val	Gly
				485					490						495
Phe	Pro	Gly	Val	Arg	Val	Thr	Asp	Glu	Ala	Gly	His	Pro	Val	Pro	Ser
			500					505					510		
Gln	Ile	Gln	Asn	Ser	Thr	Glu	Thr	Pro	Ser	Ala	Tyr	Asp	Leu	Leu	Ile
		515					520					525			
Leu	Thr	Thr	Ile	Pro	Gly	Leu	Ser	Tyr	Arg	His	Tyr	Asn	Ile	Arg	Pro
530						535					540				
Thr	Ala	Gly	Ala	Gln	Glu	Gly	Thr	Gln	Glu	Pro	Ala	Ala	Thr	Val	Ala
545					550					555					560
Ser	Thr	Leu	Gln	Phe	Gly	Arg	Arg	Leu	Arg	Arg	Arg	Thr	Ser	His	Ala
				565					570					575	
Gly	Arg	Tyr	Leu	Val	Pro	Val	Ala	Asn	Asp	Cys	Tyr	Ile	Val	Leu	Leu
			580					585					590		
Asp	Gln	Asp	Thr	Asn	Leu	Met	His	Ser	Ile	Trp	Glu	Arg	Gln	Ser	Asn
		595					600					605			
Arg	Thr	Val	Arg	Val	Thr	Gln	Glu	Phe	Leu	Glu	Tyr	His	Val	Asn	Gly
		610				615					620				
Asp	Val	Lys	Gln	Gly	Pro	Ile	Ser	Asp	Asn	Tyr	Leu	Phe	Thr	Pro	Gly
625					630					635					640
Lys	Ala	Ala	Val	Pro	Ala	Trp	Glu	Ala	Val	Glu	Met	Glu	Ile	Val	Ala
				645					650					655	
Gly	Gln	Leu	Val	Thr	Glu	Ile	Arg	Gln	Tyr	Phe	Tyr	Arg	Asn	Met	Thr
			660					665					670		
Ala	Gln	Asn	Tyr	Thr	Tyr	Ala	Ile	Arg	Ser	Arg	Leu	Thr	His	Val	Pro
		675					680					685			
Gln	Gly	His	Asp	Gly	Glu	Leu	Leu	Cys	His	Arg	Ile	Glu	Gln	Glu	Tyr
690						695					700				
Gln	Ala	Gly	Pro	Leu	Glu	Leu	Asn	Arg	Glu	Ala	Val	Leu	Arg	Thr	Ser
705					710					715					720
Thr	Asn	Leu	Asn	Ser	Gln	Gln	Val	Ile	Tyr	Ser	Asp	Asn	Asn	Gly	Tyr
				725					730					735	
Gln	Met	Gln	Arg	Pro	Tyr	Val	Ser	Tyr	Val	Asn	Asn	Ser	Ile	Ala	
			740					745					750		
Arg	Asn	Tyr	Tyr	Pro	Met	Val	Gln	Ser	Ala	Phe	Met	Glu	Asp	Gly	Lys

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      755              760              765
Ser Arg Leu Val Leu Leu Ser Glu Arg Ala His Gly Ile Ser Ser Gln
770              775              780
Gly Asn Gly Gln Val Glu Val Met Leu His Arg Arg Leu Trp Asn Asn
785              790              795              800
Phe Asp Trp Asp Leu Gly Tyr Asn Leu Thr Leu Asn Asp Thr Ser Val
805              810              815
Val His Pro Val Leu Trp Leu Leu Leu Gly Ser Trp Ser Leu Thr Thr
820              825              830
Ala Leu Arg Gln Arg Ser Ala Leu Ala Leu Gln His Arg Pro Val Val
835              840              845
Leu Phe Gly Asp Leu Ala Gly Thr Ala Pro Lys Leu Pro Gly Pro Gln
850              855              860
Gln Gln Glu Ala Val Thr Leu Pro Pro Asn Leu His Leu Gln Ile Leu
865              870              875              880
Ser Ile Pro Gly Trp Arg Tyr Ser Ser Asn His Thr Glu His Ser Gln
885              890              895
Asn Leu Arg Lys Gly His Arg Gly Glu Ala Gln Ala Asp Leu Arg Arg
900              905              910
Val Leu Leu Arg Leu Tyr His Leu Tyr Glu Val Gly Glu Asp Pro Val
915              920              925
Leu Ser Gln Pro Val Thr Val Asn Leu Glu Ala Val Leu Gln Ala Leu
930              935              940
Gly Ser Val Val Ala Val Glu Glu Arg Ser Leu Thr Gly Thr Trp Asp
945              950              955              960
Leu Ser Met Leu His Arg Trp Ser Trp Arg Thr Gly Pro Gly Arg His
965              970              975
Arg Gly Asp Thr Thr Ser Pro Ser Arg Pro Pro Gly Gly Pro Ile Ile
980              985              990
Thr Val His Pro Lys Glu Ile Arg Thr Phe Phe Ile His Phe Gln Gln
995              1000              1005
Gln

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<210> 48
<211> 104
<212> PRT
<213> Homo sapiens

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      <400> 48
Met Ala Lys Ile Ser Phe Ser Thr Glu Thr Ala Arg Cys Ile Glu Ser
1      5      10      15
Leu Ile Ala Val Phe Gln Lys Tyr Ala Gly Lys Asp Gly Tyr Asn Cys
20      25      30
Asn Leu Ser Lys Thr Glu Phe Pro Ser Phe Met Asn Lys Glu Leu Ala
35      40      45
Ala Phe Thr Lys Asn Gln Lys Asp Pro Gly Val Leu Asp Arg Met Lys
50      55      60
Lys Leu Ala Val Ser Ser Asp Gly Lys Leu Asp Phe Pro Lys Phe Leu
65      70      75      80
Asn Leu Ile Gly Gly Leu Ala Ala Ala Cys His Asp Ser Phe Leu Lys
85      90      95
Ala Val Pro Ser Gln Lys Trp Asn
100

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<210> 49
<211> 102
<212> PRT
<213> Homo sapiens

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<400> 49  
 Met Glu Lys Phe Ser Ser Pro Thr Glu Thr Glu Gln Cys Ile Lys Ser  
 1 5 10 15  
 Leu Ile Ala Ile Phe Gln Glu Asp Ala Gly Lys Asp Val Thr Thr Ala  
 20 25 30  
 Asn Ser Pro Arg Gly Glu Pro Leu Ser Phe Met Asn Thr Glu Leu Ala  
 35 40 45  
 Ala Leu Thr Gln Asn His Lys Asp Ala Gly Val Leu Asp His Met Met  
 50 55 60  
 Lys Lys Leu Asp Leu Asn Cys Asp Arg Gln Leu Asp Phe Gln Glu Leu  
 65 70 75 80  
 Leu Asn Leu Phe Cys Phe Pro His Leu Arg Leu Lys Asn Phe Leu Ile  
 85 90 95  
 Leu Leu Ala Ala Trp Pro  
 100

<210> 50  
 <211> 716  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Asn Ser Phe Arg Ala Ala Ile Leu Phe Trp Thr Val Ala Ala Trp  
 1 5 10 15  
 Val Thr Ser Gly Lys Pro Leu Gly Glu Thr Asp Glu Val Gly Phe Gln  
 20 25 30  
 Lys Cys Lys Asp Ala Trp Lys Leu Pro Ile Leu Glu Val Leu Ser Gly  
 35 40 45  
 Gly Gly Trp Asp Asn Leu Arg Asn Val Asp Met Gly Trp Val Met Asp  
 50 55 60  
 Leu Thr Tyr Thr Asn Cys Arg Thr Thr Glu Asp Gly Gln Tyr Ile Ile  
 65 70 75 80  
 Pro Asp Glu Ile Phe Thr Ile Leu Gln Lys Gln Ser Asn Leu Glu Met  
 85 90 95  
 Asn Ser Glu Ile Leu Glu Ser Trp Val Asn Tyr Gln Arg Ser Ile Ser  
 100 105 110  
 Tyr Tyr Ile Asn Thr Asp Leu Cys Leu Tyr Ser Lys Val Asn Ala Lys  
 115 120 125  
 Phe Ser Ala Glu Phe Gln Arg Met Lys Thr Leu Gln Val Lys Asp Lys  
 130 135 140  
 Ala Ile Thr Thr Arg Val Gln Val Arg Asn Leu Val Tyr Thr Val Lys  
 145 150 155 160  
 Ile Asn Pro Thr Leu Glu Leu Ser Ser Gly Phe Arg Lys Glu Leu Leu  
 165 170 175  
 Asp Ile Ser Asp Cys Leu Glu Asn Asn Gln Arg Arg Met Ala Thr Tyr  
 180 185 190  
 Leu Ala Glu Leu Leu Val Leu Asn Tyr Gly Thr His Val Ile Thr Ser  
 195 200 205  
 Val Asp Ala Gly Ala Ala Leu Ile Gln Glu Asp His Ile Lys Ala Ser  
 210 215 220  
 Phe Phe Gln Asp Ser Gln Ser Ser Arg Ser Ala Val Thr Ala Ser Ala  
 225 230 235 240  
 Gly Leu Ala Phe Gln Asn Thr Val Asn Phe Thr Phe Glu Glu Asn His  
 245 250 255  
 Thr Ser Glu Asn Val Leu Thr Lys Ser Tyr Leu Ser Asn Arg Thr Asn  
 260 265 270  
 Ser Arg Val Gln Ser Ile Gly Gly Val Pro Phe Tyr Pro Gly Ile Thr  
 275 280 285

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Leu Gln Ala Trp Gln Gln Gly Ile Thr Asn His Leu Val Ala Ile Asp
290                295                300
Arg Ser Gly Leu Pro Leu His Phe Phe Ile Asn Pro Asn Met Leu Pro
305                310                315                320
Asp Leu Pro Gly Pro Leu Val Lys Lys Val Ser Lys Thr Val Glu Thr
325                330                335
Ala Val Lys Arg Tyr Tyr Thr Phe Asn Thr Asn Pro Gly Cys Thr Asp
340                345                350
Leu Asn Ser Pro Tyr Phe Asn Phe Gln Ala Asn Thr Asp Asp Val Ser
355                360                365
Cys Glu Gly Lys Met Thr Asn Phe Ser Phe Val Gly Val Tyr Gln Lys
370                375                380
Cys Ser Gln Phe Ser Gly Asn Lys Asn Val Val Leu Cys Pro Lys Leu
385                390                395                400
Glu Gln Lys Asn Pro Leu Thr Gly Asp Phe Ser Cys Pro Ser Gly Cys
405                410                415
Ser Ser Val His Leu Leu Ser Lys Thr Cys Glu Glu Cys Cys Asn His
420                425                430
Leu Glu Cys His Lys Lys Cys Thr Leu Leu Val Phe Cys Lys Thr Val
435                440                445
Cys Glu Asp Val Phe Gln Ala Ala Lys Gly Glu Phe Arg Ala Phe Trp
450                455                460
Cys Val Ala Ser Ser Gln Val Pro Asp Asn Ser Gly Leu Leu Phe Arg
465                470                475                480
Gly Leu Phe Asn Ser Lys Ser Ile Asn Pro Met Thr Asn Ala Gln Ser
485                490                495
Cys Pro Thr Gly Tyr Phe Pro Trp Arg Leu Phe Glu Asn Leu Lys Val
500                505                510
Cys Val Ser Gln Asp Tyr Glu Leu Gly Ser Arg Phe Ala Val Pro Phe
515                520                525
Gly Gly Phe Phe Ser Cys Thr Val Gly Asn Pro Leu Val Val Pro Ala
530                535                540
Thr Ser Lys Asp Leu Gly Ala Pro Ser Leu Lys Lys Cys Pro Arg Gly
545                550                555                560
Phe Ser Gln His Leu Ala Leu Ile Ser Asn Gly Cys Gln Val Ser Tyr
565                570                575
Cys Val Lys Ala Gly Leu Phe Thr Glu Lys Phe Leu Pro Pro Ala Ser
580                585                590
Leu Pro Pro Phe Thr Gln Pro Pro Leu Met Ser Glu Ala Asp Ala Asn
595                600                605
Thr Val Ile Val Thr Ser Ser Glu Asn Ala Arg Ser Trp Ile Lys Asp
610                615                620
Ser Gln Thr His Gln Trp Arg Leu Gly Glu Gln Leu Glu Leu Arg Ser
625                630                635                640
Thr Met Ser Ala Ile His Lys Asp Gly Gly Gly Leu Ser Gly Gly Ala
645                650                655
Thr Ala Gly Ile Val Val Gly Ala Thr Thr Ile Leu Ala Val Val Ile
660                665                670
Thr Leu Ala Ile Cys Gly Thr Arg Lys Phe Lys Lys Arg Gly Tyr Leu
675                680                685
Ala Phe Trp Lys Arg Gln Ser Leu Val Pro Gly Thr Ala Ala Thr Gly
690                695                700
Asp Asn Pro Asp Glu Glu Gln Gly Gln Ser Pro Ala
705                710                715

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&lt;210&gt; 51

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 51  
Met Asn Asn Phe Arg Ala Thr Ile Leu Phe Trp Ala Ala Ala Ala Trp  
1 5 10 15  
Ala Lys Ser Gly Lys Pro Ser Gly Glu Met Asp Glu Val Gly Val Gln  
20 25 30  
Lys Cys Lys Asn Ala Leu Lys Leu Pro Val Leu Glu Val Leu Pro Gly  
35 40 45  
Gly Gly Trp Asp Asn Leu Arg Asn Val Asp Met Gly Arg Val Met Glu  
50 55 60  
Leu Thr Tyr Ser Asn Cys Arg Thr Thr Glu Asp Gly Gln Tyr Ile Ile  
65 70 75 80  
Pro Asp Glu Ile Phe Thr Ile Pro Gln Lys Gln Ser Asn Leu Glu Met  
85 90 95  
Asn Ser Glu Ile Leu Glu Ser Trp Ala Asn Tyr Gln Ser Ser Thr Ser  
100 105 110  
Tyr Ser Ile Asn Thr Glu Leu Ser Leu Phe Ser Lys Val Asn Gly Lys  
115 120 125  
Phe Ser Thr Glu Phe Gln Arg Met Lys Thr Leu Gln Val Lys Asp Gln  
130 135 140  
Ala Ile Thr Thr Arg Val Gln Val Arg Asn Leu Val Tyr Thr Val Lys  
145 150 155 160  
Ile Asn Pro Thr Leu Glu Leu Ser Ser Gly Phe Arg Lys Glu Leu Leu  
165 170 175  
Asp Ile Ser Asp Arg Leu Glu Asn Asn Gln Thr Arg Met Ala Thr Tyr  
180 185 190  
Leu Ala Glu Leu Leu Val Leu Asn Tyr Gly Thr His Val Thr Thr Ser  
195 200 205  
Val Asp Ala Gly Ala Ala Leu Ile Gln Glu Asp His Leu Arg Ala Ser  
210 215 220  
Phe Leu Gln Asp Ser Gln Ser Ser Arg Ser Ala Val Thr Ala Ser Ala  
225 230 235 240  
Gly Leu Ala Phe Gln Asn Thr Val Asn Phe Lys Phe Glu Glu Asn Tyr  
245 250 255  
Thr Ser Gln Asn Val Leu Thr Lys Ser Tyr Leu Ser Asn Arg Thr Asn  
260 265 270  
Ser Arg Val Gln Ser Ile Gly Gly Val Pro Phe Tyr Pro Gly Ile Thr  
275 280 285  
Leu Gln Ala Trp Gln Gln Gly Ile Thr Asn His Leu Val Ala Ile Asp  
290 295 300  
Arg Ser Gly Leu Pro Leu His Phe Phe Ile Asn Pro Asn Met Leu Pro  
305 310 315 320  
Asp Leu Pro Gly Pro Leu Val Lys Lys Val Ser Lys Thr Val Glu Thr  
325 330 335  
Ala Val Lys Arg Tyr Tyr Thr Phe Asn Thr Tyr Pro Gly Cys Thr Asp  
340 345 350  
Leu Asn Ser Pro Asn Phe Asn Phe Gln Ala Asn Thr Asp Asp Gly Ser  
355 360 365  
Cys Glu Gly Lys Met Thr Asn Phe Ser Phe Gly Gly Val Tyr Gln Glu  
370 375 380  
Cys Thr Gln Leu Ser Gly Asn Arg Asp Val Leu Cys Gln Lys Leu  
385 390 395 400  
Glu Gln Lys Asn Pro Leu Thr Gly Asp Phe Ser Cys Pro Ser Gly Tyr  
405 410 415  
Ser Pro Val His Leu Leu Ser Gln Ile His Glu Glu Gly Tyr Asn His  
420 425 430  
Leu Glu Cys His Arg Lys Cys Thr Leu Leu Val Phe Cys Lys Thr Val  
435 440 445  
Cys Glu Asp Val Phe Gln Val Ala Lys Ala Glu Phe Arg Ala Phe Trp

450		455		460
Cys Val Thr Ser Ser Gln	Val Pro Glu Asn Ser Gly	Leu Leu Phe Gly		
465		470		480
Gly Leu Phe Ser Ser Lys	Ser Ile Asn Pro Met Thr	Asn Ala Gln Ser		
	485		490	495
Cys Pro Ala Gly Tyr Phe	Pro Leu Arg Leu Phe	Glu Asn Leu Lys Val		
	500		505	510
Cys Val Ser Gln Asp Tyr	Glu Leu Gly Ser Arg Phe	Ala Val Pro Phe		
	515		520	525
Gly Gly Phe Phe Ser Cys	Thr Val Gly Asn Pro Leu	Val Asp Pro Ala		
	530		535	540
Ile Ser Arg Asp Leu Gly	Ala Pro Ser Leu Lys Lys	Cys Pro Gly Gly		
545		550		560
Phe Ser Gln His Pro Ala	Leu Ile Ser Asp Gly Cys	Gln Val Ser Tyr		
	565		570	575
Cys Val Lys Ser Gly Leu	Phe Thr Gly Gly Ser Leu	Pro Pro Ala Arg		
	580		585	590
Leu Pro Pro Phe Thr Arg	Pro Pro Leu Met Ser Gln	Ala Ala Thr Asn		
	595		600	605
Thr Val Ile Val Thr Asn	Ser Glu Asn Ala Arg Ser	Trp Ile Lys Asp		
	610		615	620
Ser Gln Thr His Gln Trp	Arg Leu Gly Glu Pro Ile	Glu Leu Arg Arg		
625		630		640
Ala Met Asn Val Ile His	Gly Met Val Val Val Cys	Gln Glu Gly Leu		
	645		650	655
Gln Leu Gly Ser Gln Trp	Gly Ser Pro Phe Trp Leu	Leu Leu Ser		
	660		665	670
Pro Trp Pro Ser Thr Ala	Pro Gly Ser Ser Arg Arg	Lys His Ile Arg		
	675		680	685
Gln Leu Arg Lys Gly Arg	Val Trp Phe Gln Ala Leu	Gln Gln Leu Glu		
	690		695	700
Thr Pro Leu Thr Lys Ser	Arg Gly Arg Val Gln Leu	Lys Ser Leu Pro		
705		710		720
Glu Asn Gly Phe Ser His	Leu Gln Cys Gly His Cys			
	725		730	

&lt;210&gt; 52

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

Met Arg Trp Pro Pro Ser	Pro Thr His His Pro	Arg Trp Gly Lys Pro
1	5	10
Gln Ala Gly Trp Val Glu	Lys Asn Leu Pro Thr	His Ser Pro Cys Ser
	20	25
Cys Phe Ile Asp Glu His	Val Thr Arg Val Ala	Trp Leu Asn Arg Ser
	35	40
Asn Ile Leu Tyr Ala Gly	Asn Asp Arg Trp Thr	Ser Asp Pro Arg Val
	50	55
Arg Leu Leu Ile Asn Thr	Pro Glu Glu Phe Ser	Ile Leu Ile Thr Glu
65	70	75
Val Gly Leu Gly Asp Glu	Gly Leu Tyr Thr Cys	Ser Phe Gln Thr Arg
	85	90
His Gln Pro Tyr Thr Thr	Gln Val Tyr Leu Ile	Val His Val Pro Ala
	100	105
Arg Ile Val Asn Ile Ser	Ser Pro Val Thr Val	Asn Glu Gly Gly Asn
	115	120
Val Asn Leu Leu Cys Leu	Ala Val Gly Arg Pro	Glu Pro Thr Val Thr
	125	

130		135		140
Trp Arg Gln Leu Arg Gly	Glu Asp Pro Ile Pro Asp Gly Phe Thr Ser			
145		150		155
Glu Gly Glu Ile Leu Glu	Ile Ser Asp Ile Gln Arg Gly Gln Ala Gly			160
	165		170	175
Glu Tyr Glu Cys Val Thr	His Asn Gly Val Asn Ser Ala Pro Asp Ser			
	180		185	190
Arg Arg Val Leu Val Thr	Val Asn Tyr Pro Pro Thr Ile Thr Asp Val			
	195		200	205
Thr Ser Ala Arg Thr Ala	Leu Gly Arg Ala Ala Leu Leu Arg Cys Glu			
	210		215	220
Ala Met Ala Val Pro Pro	Ala Asp Phe Gln Trp Tyr Lys Asp Asp Arg			
225		230		235
Leu Leu Ser Ser Gly Thr	Ala Glu Gly Leu Lys Val Gln Thr Glu Arg			
	245		250	255
Thr Arg Ser Met Leu Leu	Phe Ala Lys Arg Glu Arg Pro Ala Leu Arg			
	260		265	270
Asn Tyr Thr Cys Arg Ala	Ser His Arg Leu Gly Ala Ser Ser Ala Ser			
	275		280	285
Met Arg Leu Leu Arg Ala	Ser Ser Gly Gly Ala Gly Pro Gly Arg Gly			
	290		295	300
Pro Gln Ala Lys Ser Glu	Arg Asn Gly Gly Ala Arg Ala Val Gly Leu			
305		310		315
Val Gly Ala Glu Glu Leu	Ser Ala Thr Lys Glu Glu Glu Arg Gly Glu			
	325		330	335
Glu Glu Glu Ala Glu Glu	Glu Arg Ser Ser Glu Asn Pro Ser Leu			
	340		345	350

&lt;210&gt; 53

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 53

Met Pro Pro Ala Ala Pro	Gly Ala Arg Leu Arg Leu Leu Ala Ala Ala
1	5 10 15
Ala Leu Ala Gly Leu Ala	Val Ile Ser Arg Gly Leu Leu Ser Gln Arg
	20 25 30
Leu Glu Phe Asn Ser Pro	Ala Asp Asn Tyr Thr Val Cys Glu Gly Asp
	35 40 45
Asn Ala Thr Leu Ser Cys	Phe Met Asp Glu His Val Thr Arg Val Ala
	50 55 60
Trp Leu Asn Arg Ser Asn	Ile Leu Tyr Ala Gly Asn Asp Arg Arg Thr
65	70 75 80
Arg Asp Pro Arg Val Arg	Leu Leu Ile Asn Thr Pro Glu Glu Phe Ser
	85 90 95
Ile Leu Val Thr Glu Val	Gly Leu Gly Asp Glu Gly Leu Tyr Thr Cys
	100 105 110
Ser Phe Gln Thr Arg His	Gln Pro Tyr Thr Thr Gln Val Tyr Leu Ile
	115 120 125
Val His Val Pro Ala Arg	Val Val Asn Ile Ser Ser Pro Val Met Val
	130 135 140
Asn Glu Gly Gly Asn Val	Asn Leu Leu Cys Leu Ala Val Gly Arg Pro
145	150 155 160
Glu Pro Thr Val Thr Trp	Arg Gln Leu Arg Asp Gly Phe Thr Ser Glu
	165 170 175
Gly Glu Ile Leu Glu Ile	Ser Asp Ile Leu Arg Gly Gln Ala Gly Glu
	180 185 190
Tyr Glu Cys Val Thr His	Asn Gly Val Asn Ser Ala Pro Asp Ser Arg



195	200	205
Arg Val Leu Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Asp Val Thr		
210	215	220
Ser Ala Arg Thr Ala Leu Gly Arg Ala Ala Leu Leu Arg Cys Glu Ala		
225	230	235
Met Ala Val Ser Pro Ala Asp Phe Gln Trp Tyr Lys Asp Asp Arg Leu		
	245	250
Leu Ser Ser Gly Thr Ala Glu Gly Leu Lys Val Gln Met Glu Arg Thr		
	260	265
Arg Ser Met Leu Leu Phe Ala Asn Met Ser Ala Arg His Tyr Gly Asn		
	275	280
Tyr Thr Cys Cys Ala Ala Asn Arg Leu Gly Ala Ser Ser Ala Ser Met		
	290	295
Arg Leu Leu Cys Pro Gly Ser Leu Glu Asn Ser Ala Pro Arg Pro Pro		
305	310	315
Gly Pro Leu Ala Leu Leu Ser Ala Leu Gly Trp Leu Trp Trp Arg Met		
	325	330
		335

&lt;210&gt; 54

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe		
1	5	10
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro		
	20	25
Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp		
	35	40
His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu		
	50	55
Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Met Ile Val Asp Lys Ile		
	65	70
Asp Ala Asp Lys Asp Gly Phe Val Thr Glu Gly Glu Leu Lys Ser Trp		
	85	90
Ile Lys His Ala Gln Lys Lys Tyr Ile Tyr Asp Asn Val Glu Asn Gln		
	100	105
Trp Gln Glu Phe Asp Met Asn Gln Asp Gly Leu Ile Ser Trp Asp Glu		
	115	120
Tyr Arg Asn Val Thr Tyr Gly Thr Tyr Leu Asp Asp Pro Asp Pro Asp		
	130	135
Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe		
	145	150
Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe		
	165	170
Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val		
	180	185
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile		
	195	200
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr		
	210	215
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe		
	225	230
Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp		
	245	250
Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His		
	260	265
Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu		
		270

275                      280                      285  
 Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp  
 290                      295                      300  
 Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe  
 305                      310                      315

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 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 55  
 Met Lys Leu Asn Leu Val Gln Ile Phe Phe Met Leu Leu Met Leu Leu  
 1                      5                      10                      15  
 Leu Gly Leu Gly Met Gly Leu Gly Leu Gly Leu His Met Ala Thr Ala  
 20                      25                      30  
 Val Leu Glu Glu Ser Asp Gln Pro Leu Asn Glu Phe Trp Ser Ser Asp  
 35                      40                      45  
 Ser Gln Asp Lys Ala Glu Ala Thr Glu Glu Gly Asp Gly Thr Gln Thr  
 50                      55                      60  
 Thr Glu Thr Leu Val Leu Ser Asn Lys Glu Val Val Gln Pro Gly Trp  
 65                      70                      75                      80  
 Pro Glu Asp Pro Ile Leu Gly Glu Asp Glu Val Gly Gly Asn Lys Met  
 85                      90                      95  
 Leu Arg Ala Ser Ala Leu Phe Gln Ser Asn Lys Asp Tyr Leu Arg Leu  
 100                      105                      110  
 Asp Gln Thr Asp Arg Glu Cys Asn Asp Met Met Ala His Lys Met Lys  
 115                      120                      125  
 Glu Pro Ser Gln Ser Cys Ile Ala Gln Tyr Ala Phe Ile His Glu Asp  
 130                      135                      140  
 Leu Asn Thr Val Lys Ala Val Cys Asn Ser Pro Val Ile Ala Cys Glu  
 145                      150                      155                      160  
 Leu Lys Gly Gly Lys Cys His Lys Ser Ser Arg Pro Phe Asp Leu Thr  
 165                      170                      175  
 Leu Cys Glu Leu Ser Gln Pro Asp Gln Val Thr Pro Asn Cys Asn Tyr  
 180                      185                      190  
 Leu Thr Ser Val Ile Lys Lys His Ile Ile Ile Thr Cys Asn Asp Met  
 195                      200                      205  
 Lys Arg Gln Leu Pro Thr Gly Gln  
 210                      215

<210> 56  
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 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Thr Pro Pro Lys Leu Arg Ala Ser Leu Ser Pro Ser Leu Leu Leu  
 1                      5                      10                      15  
 Leu Leu Ser Gly Cys Leu Leu Ala Ala Ala Arg Arg Glu Lys Gly Ala  
 20                      25                      30  
 Ala Ser Asn Val Ala Glu Pro Val Pro Gly Pro Pro Gly Gly Ser Ser  
 35                      40                      45  
 Gly Arg Phe Leu Ser Pro Glu Gln His Ala Cys Ser Trp Gln Leu Leu  
 50                      55                      60  
 Leu Pro Ala Pro Glu Ala Ala Ala Gly Ser Glu Leu Ala Leu Arg Cys  
 65                      70                      75                      80  
 Gln Ser Pro Asp Gly Ala Arg His Gln Cys Ala Tyr Arg Gly His Pro  
 85                      90                      95

Glu	Arg	Cys	Ala	Ala	Tyr	Ala	Ala	Arg	Arg	Ala	His	Phe	Trp	Lys	Gln
			100					105					110		
Val	Leu	Gly	Gly	Leu	Arg	Lys	Lys	Arg	Arg	Pro	Cys	His	Asp	Pro	Ala
		115					120					125			
Pro	Leu	Gln	Ala	Arg	Leu	Cys	Ala	Gly	Lys	Lys	Gly	His	Gly	Ala	Glu
		130				135					140				
Leu	Arg	Leu	Val	Pro	Arg	Ala	Ser	Pro	Pro	Ala	Arg	Pro	Thr	Val	Ala
145					150					155					160
Gly	Phe	Ala	Gly	Glu	Ser	Lys	Pro	Arg	Ala	Arg	Asn	Arg	Gly	Arg	Thr
				165					170					175	
Arg	Glu	Arg	Ala	Ser	Gly	Pro	Ala	Ala	Gly	Thr	Pro	Pro	Pro	Gln	Ser
			180					185					190		
Ala	Pro	Pro	Lys	Glu	Asn	Pro	Ser	Glu	Arg	Lys	Thr	Asn	Glu	Gly	Lys
		195					200					205			
Arg	Lys	Ala	Ala	Leu	Val	Pro	Asn	Glu	Glu	Arg	Pro	Met	Gly	Thr	Gly
		210				215					220				
Pro	Asp	Pro	Asp	Gly	Leu	Asp	Gly	Asn	Ala	Glu	Leu	Thr	Glu	Thr	Tyr
225					230					235					240
Cys	Ala	Glu	Lys	Trp	His	Ser	Leu	Cys	Asn	Phe	Phe	Val	Asn	Phe	Trp
				245					250					255	
Asn	Gly														

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